

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 13, 2005, 12:13:19 ; Search time 161 Seconds

(without alignments)

40.793 Million cell updates/sec

Title: US-09-647-457E-1
perfect score: 83

Sequence: 1 LVVGLCTXQIKTGPACKX 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1726220 seqs, 386332138 residues

Total number of hits satisfying chosen parameters: 1726220

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Published Applications An:*

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21: /cgmn_6/ptodata/1/pubpa/US11D_PUBCOMB.pep:*

22: /cgmn_6/ptodata/1/pubpa/US11E_PUBCOMB.pep:*

ALIGNMENTS

RESULT 1

US-10-733-969A-13
; Sequence 13, Application US/10733969A

; Publication No. US2004021957A1

; GENERAL INFORMATION:

; APPLICANT: CHEN, JIE

; APPLICANT: HU, LIPING

; APPLICANT: LIU, TONG HUA

; APPLICANT: LU, ZHENG HUI

; APPLICANT: SHEN, YAN

; TITLE OF INVENTION: SPECIFIC MARKERS FOR PANCRATIC CANCER

; FILE REFERENCE: 21525

; CURRENT APPLICATION NUMBER: US/10/733,969A

; CURRENT FILING DATE: 2003-12-11

; PRIORITY APPLICATION NUMBER: EP 0228059, 2

; PRIORITY FILING DATE: 2003-12-17

; NUMBER OF SEQ ID NOS: 110

; SOFTWARE: Patentin version 3.2

; SEQ ID NO 13

; LENGTH: 458

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURES:

; OTHER INFORMATION: Alpha enolase; Accession No: as of 06 Dec 2002: Q05524

US-10-733-969A-13

Query Match 91.6%; Score 76; DB 16; Length 458;
Best Local Similarity 87.5%; Pred. No. 0.0008; 2; Indels 0; Gaps 0;

Matches 14; Conservative 0; Mismatches 0;

QY 1 LVVGLCTXQIKTGAC 16

Db 407 LVVGLCTXQIKTGTC 422

Pred. No. 1 is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	76	91.6	458	Sequence 13, Appl
2	76	91.6	458	Sequence 6, Appl
3	67	80.7	50	Sequence 325, Appl
4	67	80.7	269	Sequence 1043, Appl
5	67	80.7	272	Sequence 1041, Appl
6	67	80.7	16	Sequence 1044, Appl
7	67	80.7	336	Sequence 1042, Appl
8	67	80.7	420	Sequence 17, Appl
9	67	80.7	429	Sequence 604, Appl
10	67	80.7	16	Sequence 9, Appl
11	67	80.7	433	Sequence 61, Appl

RESULT 2 ;
US-10-478-519-6 ;
; Sequence 6, Application US/10478519
; Publication No. US20050042738A1
; GENERAL INFORMATION:
; APPLICANT: SWARNAKAR, Anita; GORVAD, Ami E.;
; APPLICANT: HAFALIA, April J.A.; DUGGAN, Brendan M.;
; APPLICANT: EMERLING, Brooke M.; ISON, Craig H.;
; APPLICANT: NGUYEN, Daniel B.; LEE, Ernestine A.;
; APPLICANT: YUE, Henry; YUE, Huibin;
; APPLICANT: FORSYTHE, Ian J.; LI, Joana X.;
; APPLICANT: THANGAVELU, Kavitha; CHAWLA, Narinder K.;
; APPLICANT: BURFORD, Neil; MASON, Patricia M.;
; APPLICANT: LAL, Preeta G.; LEB, Sally;
; APPLICANT: BRCHA, Shanya D.; TANG, Y. Tom
; TITLE OF INVENTION: Carbohydrate-Associated Proteins
; FILE REFERENCE: PF-0982 USN
; CURRENT APPLICATION NUMBER: US/10/478,519
; CURRENT FILING DATE: 2003-11-21
; PRIORITY APPLICATION NUMBER: PCT/US02/18354
; PRIORITY FILING DATE: 2002-05-22
; PRIORITY APPLICATION NUMBER: US 60/293,768
; PRIORITY FILING DATE: 2001-05-25
; PRIORITY APPLICATION NUMBER: US 60/309,548
; PRIORITY FILING DATE: 2001-08-01
; PRIORITY APPLICATION NUMBER: US 60/314,400
; PRIORITY FILING DATE: 2001-08-23
; PRIORITY APPLICATION NUMBER: US 60/343,706
; PRIORITY FILING DATE: 2001-10-19
; PRIORITY APPLICATION NUMBER: US 60/337,999
; PRIORITY FILING DATE: 2001-12-07
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PERL Program
; SEQ ID NO 6
; LENGTH: 458
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 7488348CD1
; US-10-478-519-6
Query Match 91.6%; Score 76; DB 17; Length 458;
Best Local Similarity 87.5%; Pred. No. 0.0008; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 2;
QY 1 LVVGLCTXQIKTGpac 16
Db 407 LVVGLCTGQIKTGPTC 422
RESULT 3 ;
US-10-776-013-325 ;
; Sequence 325, Application US/10776013
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026W01
; CURRENT APPLICATION NUMBER: US/10/473,127
; CURRENT FILING DATE: 2003-09-26
; PRIORITY APPLICATION NUMBER: 60/279,495
; PRIORITY FILING DATE: 2001-03-28
; PRIORITY APPLICATION NUMBER: 60/292,544
; PRIORITY FILING DATE: 2001-05-21
; PRIORITY APPLICATION NUMBER: 60/310,801
; PRIORITY FILING DATE: 2001-08-08
; PRIORITY APPLICATION NUMBER: 60/326,370
; PRIORITY FILING DATE: 2001-10-01
; PRIORITY APPLICATION NUMBER: 60/336,780
; PRIORITY FILING DATE: 2001-12-04
; PRIORITY APPLICATION NUMBER: 60/358,985
; PRIORITY FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSBQ for Windows Version 4.0
; SEQ ID NO 1043
; LENGTH: 269
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-473-127-1043
Query Match 80.7%; Score 67; DB 16; Length 269;
Best Local Similarity 81.2%; Pred. No. 0.013; Indels 0; Gaps 0;
Matches 13; Conservative 0; Mismatches 3;
QY 1 LVVGLCTXQIKTGpac 16
Db 219 LVVGLCTGQIKTGpac 234
RESULT 4 ;
US-10-473-127-1043 ;
; Sequence 1043, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026W01
; CURRENT APPLICATION NUMBER: US/10/473,127
; CURRENT FILING DATE: 2003-09-26
; PRIORITY APPLICATION NUMBER: 60/279,495
; PRIORITY FILING DATE: 2001-03-28
; PRIORITY APPLICATION NUMBER: 60/292,544
; PRIORITY FILING DATE: 2001-05-21
; PRIORITY APPLICATION NUMBER: 60/310,801
; PRIORITY FILING DATE: 2001-08-08
; PRIORITY APPLICATION NUMBER: 60/326,370
; PRIORITY FILING DATE: 2001-10-01
; PRIORITY APPLICATION NUMBER: 60/336,780
; PRIORITY FILING DATE: 2001-12-04
; PRIORITY APPLICATION NUMBER: 60/358,985
; PRIORITY FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSBQ for Windows Version 4.0
; SEQ ID NO 1043
; LENGTH: 269
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-473-127-1043
Query Match 80.7%; Score 67; DB 16; Length 269;
Best Local Similarity 81.2%; Pred. No. 0.013; Indels 0; Gaps 0;
Matches 13; Conservative 0; Mismatches 3;
QY 1 LVVGLCTXQIKTGpac 16
Db 219 LVVGLCTGQIKTGpac 234
RESULT 5 ;
US-10-473-127-1041 ;
; Sequence 1041, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.


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; TITLE OF INVENTION: Endometrium
; FILE REFERENCE: 8969-014
; CURRENT APPLICATION NUMBER: US/09/935,642
; CURRENT FILING DATE: 2001-08-24
; PRIORITY APPLICATION NUMBER: PCT/GB97/023394
; PRIORITY FILING DATE: 1997-09-05
; PRIORITY APPLICATION NUMBER: PCT/GB97/132.8
; PRIORITY FILING DATE: 1997-04-08
; PRIORITY APPLICATION NUMBER: PCT/GB9618600.2
; PRIORITY FILING DATE: 1996-09-06
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 9
; LENGTH: 433
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE: misc_feature
; OTHER INFORMATION: Incyte ID No: 7506054CDI
; US-10-498-788-17

Query Match          80.7%; Score 67; DB 17; Length 420;
Best Local Similarity 81.2%; Pred. No. 0.02; Mismatches 3; Indels 0; Gaps 0;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy      1 LVVGLCTXQIKTGAPC 16
Db      370 LVVGLCTXQIKTGAPC 385

RESULT 9
US-10-473-127-604
; Sequence 604, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026W01
; CURRENT APPLICATION NUMBER: US/10/473,127
; CURRENT FILING DATE: 2003-09-26
; PRIORITY APPLICATION NUMBER: 60/279,495
; PRIORITY FILING DATE: 2001-03-28
; PRIORITY APPLICATION NUMBER: 60/292,544
; PRIORITY FILING DATE: 2001-05-21
; PRIORITY APPLICATION NUMBER: 60/310,801
; PRIORITY FILING DATE: 2001-08-08
; PRIORITY APPLICATION NUMBER: 60/326,370
; PRIORITY FILING DATE: 2001-10-01
; PRIORITY APPLICATION NUMBER: 60/336,780
; PRIORITY FILING DATE: 2001-12-04
; PRIORITY APPLICATION NUMBER: 60/358,985
; PRIORITY FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 604
; LENGTH: 420
; TYPE: PRT
; ORGANISM: Homo sapiens

Query Match          80.7%; Score 67; DB 17; Length 429;
Best Local Similarity 81.2%; Pred. No. 0.021; Mismatches 3; Indels 0; Gaps 0;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy      1 LVVGLCTXQIKTGAPC 16
Db      379 LVVGLCTXQIKTGAPC 394

RESULT 10
US-09-935-642-9
; Sequence 9, Application US/09935642
; Publication No. US2003004755A1
; GENERAL INFORMATION:
; APPLICANT: BYRJALSEN, Inger
; APPLICANT: LARSEN, Peter
; APPLICANT: STEPHEN, John
; TITLE OF INVENTION: Biochemical Markers for the Human

Query Match          80.7%; Score 67; DB 16; Length 420;
Best Local Similarity 81.2%; Pred. No. 0.021; Mismatches 3; Indels 0; Gaps 0;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy      1 LVVGLCTXQIKTGAPC 16
Db      379 LVVGLCTXQIKTGAPC 394

RESULT 11
US-10-733-969A-61
; Sequence 61, Application US/10733969A
; Publication No. US20040219572A1
; GENERAL INFORMATION:
; APPLICANT: CHEN, JIE
; APPLICANT: HU, LIPING
; APPLICANT: LIU, TONG HUA
; APPLICANT: LU, ZHAO HUI
; APPLICANT: SHEN, YAN
; TITLE OF INVENTION: SPECIFIC MARKERS FOR PANCRATIC CANCER
; FILE REFERENCE: 21525
; CURRENT APPLICATION NUMBER: US/10/733,969A
; CURRENT FILING DATE: 2003-12-11
; PRIORITY APPLICATION NUMBER: EP 02028088.2
; PRIORITY FILING DATE: 2002-12-17
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: Patentin version 3.2
; SEQ ID NO: 61
; LENGTH: 433
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE: misc_feature
; OTHER INFORMATION: human alpha enolase; Accession No: P06733
; OTHER INFORMATION: as of 29 August 2003: P06733
; US-10-733-969A-61

Query Match          80.7%; Score 67; DB 16; Length 433;
Best Local Similarity 81.2%; Pred. No. 0.021; Mismatches 3; Indels 0; Gaps 0;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy      1 LVVGLCTXQIKTGAPC 16
Db      383 LVVGLCTXQIKTGAPC 398

RESULT 12
US-10-473-127-608
; Sequence 608, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026W01
; CURRENT APPLICATION NUMBER: US/10/473,127

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; PRIOR APPLICATION NUMBER: 60/279,495
 ; PRIOR FILING DATE: 2001-03-28
 ; PRIOR APPLICATION NUMBER: 60/292,544
 ; PRIOR FILING DATE: 2001-05-21
 ; PRIOR APPLICATION NUMBER: 60/310,801
 ; PRIOR FILING DATE: 2001-08-08
 ; PRIOR APPLICATION NUMBER: 60/326,370
 ; PRIOR FILING DATE: 2001-10-01
 ; PRIOR APPLICATION NUMBER: 60/336,780
 ; PRIOR FILING DATE: 2001-12-04
 ; PRIOR APPLICATION NUMBER: 60/358,985
 ; PRIOR FILING DATE: 2002-02-20
 ; NUMBER OF SEQ ID NOS: 2011
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 608
 ; LENGTH: 433
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-473-127-608

Query Match 80.7%; Score 67; DB 16; Length 433;
 Best Local Similarity 81.2%; Pred. No. 0.021; Mismatches 3; Indels 0; Gaps 0;
 Matches 13; Conservative 0; MisMatches 3; Indels 0; Gaps 0;

Qy 1 LVVGLCTQIKTGAC 16
 Db 383 LVVGLCTQIKTGAC 398

RESULT 13
 US-10-473-127-610
 ; Sequence 610, Application US/10473127
 ; Publication No. US20040236091A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Zycos Inc.
 ; TITLE OF INVENTION: TRANSLATIONAL PROFILING
 ; FILE REFERENCE: 08191-026W01
 ; CURRENT APPLICATION NUMBER: US/10/473,127
 ; CURRENT FILING DATE: 2003-09-26
 ; PRIOR APPLICATION NUMBER: 60/279,495
 ; PRIOR FILING DATE: 2001-03-28
 ; PRIOR APPLICATION NUMBER: 60/292,544
 ; PRIOR FILING DATE: 2001-05-21
 ; PRIOR APPLICATION NUMBER: 60/311,801
 ; PRIOR FILING DATE: 2001-08-08
 ; PRIOR APPLICATION NUMBER: 60/326,370
 ; PRIOR FILING DATE: 2001-10-01
 ; PRIOR APPLICATION NUMBER: 60/336,780
 ; PRIOR FILING DATE: 2001-12-04
 ; PRIOR APPLICATION NUMBER: 60/358,985
 ; PRIOR FILING DATE: 2002-02-20
 ; NUMBER OF SEQ ID NOS: 2041
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 610
 ; LENGTH: 433
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-473-127-610

Query Match 80.7%; Score 67; DB 16; Length 433;
 Best Local Similarity 81.2%; Pred. No. 0.021; Mismatches 3; Indels 0; Gaps 0;
 Matches 13; Conservative 0; MisMatches 3; Indels 0; Gaps 0;

Qy 1 LVVGLCTQIKTGAC 16
 Db 383 LVVGLCTQIKTGAC 398

RESULT 14
 US-10-177-293-124
 ; Sequence 47, Application US/10205194
 ; Publication No. US20030134301A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Warner-Lambert Company
 ; APPLICANT: Warner-Lambert Company
 ; APPLICANT: Lee, Kevin
 ; APPLICANT: Dixon, Alastair
 ; APPLICANT: Brookbank, Robert
 ; APPLICANT: Pincock, Robert
 ; APPLICANT: Identification and Use of Molecules Implicated in Pain
 ; TITLE OF INVENTION: Identification and Use of Molecules Implicated in Pain
 ; FILE REFERENCE: WO-A-018201
 ; CURRENT APPLICATION NUMBER: US/10/205,194
 ; CURRENT FILING DATE: 2001-07-24
 ; PRIOR APPLICATION NUMBER: GB 0118354.0
 ; NUMBER OF SEQ ID NOS: 177
 ; SOFTWARE: Patentin Ver. 2.1
 ; SEQ ID NO: 47
 ; LENGTH: 434
 ; TYPE: PRT

RESULT 14
 US-10-177-293-124
 ; Sequence 124, Application US/10177293
 ; Publication No. US20030124128A1
 ; GENERAL INFORMATION:

; ORGANISM: *Rattus norvegicus*
; FEATURE:
; OTHER INFORMATION: Neuron-specific enolase
US-10-205-194-47

Query Match 80.7%; Score 67; DB 14; Length 434;
Best Local Similarity 81.2%; Pred. No. 0.021; Mismatches 3; Indels 0; Gaps 0;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy	1	LWVGLCTKQIKTGAPC	16
Db	384	LWVGLCTQIKTGAPC	399

Search completed: July 13, 2005, 12:26:54
Job time : 162 secs

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OM protein - protein search, using SW model

Run on: July 13, 2005, 12:03:53 ; Search time 56 Seconds
(without alignments)
155.453 Million cell updates/sec

Title: US-09-647-457E-1
Perfect Score: 83
Sequence: 1 LVWGLCTXQIKTGPACKX 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03;*

1: uniprot_sprot;*

2: uniprot_trembl;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
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3	67	80.7	395	2 Q8046	Q8046 icterurus p
4	67	80.7	154	2 Q9NBL4	Q9nbl4 homo sapien
5	67	80.7	159	2 Q9NG70	Q9ng70 peripatus s
6	67	80.7	184	2 Q66GVL	Q66gv1 homo sapien
7	67	80.7	259	2 Q7Z2M5	Q7z2m5 sparaxis aura
8	67	80.7	264	2 Q8WU71	Q8wu71 homo sapien
9	67	80.7	272	2 Q8B962	Q8b962 homo sapien
10	67	80.7	336	2 Q7IV37	Q7iv37 homo sapien
11	67	80.7	338	2 Q922A0	Q922a0 mus musculus
12	67	80.7	341	2 Q6GMP2	Q6gmp2 homo sapien
13	67	80.7	353	2 Q9KKT7	Q9kt7 mus musculus
14	67	80.7	366	2 Q6P1C1	Q6p1c1 mus musculus
15	67	80.7	374	2 Q65BM5	Q65bm5 homo sapien
16	67	80.7	377	2 Q6LUD3	Q6lud3 anas platyrhynchos
17	67	80.7	383	2 Q9Ng67	Q9ng67 tomocerus s
18	67	80.7	394	2 Q9PTX5	Q9ptx5 lampris re
19	67	80.7	395	1 ENO_ALUMI	F42897 alligator m
20	67	80.7	395	2 Q9PTX5	Q9ptx5 lampetra re
21	67	80.7	395	2 Q9UF57	Q9uf57 eptatretus
22	67	80.7	432	2 Q61QF5	Q61qf5 brachydanio
23	67	80.7	432	2 Q6PR12	Q6pc12 brachydanio
24	67	80.7	433	1 ENO_ALUMI	Q9pvk2 alligator m
25	67	80.7	433	1 ENO_ANAPL	F19140 anas platyrhynchos
26	67	80.7	433	1 ENOA_CHICK	P51913 gallus gallus
27	67	80.7	433	1 ENO_HUMAN	P06733 homo sapiens
28	67	80.7	433	1 ENO_MOUSE	P17182 mus musculus
29	67	80.7	433	1 ENO_PYTRG	Q9w710 python regius
30	67	80.7	433	1 ENO_RAT	Q94764 rattus norvegicus
31	80.7	433	1 ENO_SCBURN	Q9w712 sceloporus	

ALIGNMENTS

32	67	80.7	433	1 ENOA_TRASC	Q9w711 trachemys s
33	67	80.7	433	1 ENOB_CHICK	P07322 gallus gallus
34	67	80.7	433	1 ENOB_HUMAN	P13929 homo sapiens
35	67	80.7	433	1 ENOB_MOUSE	P21550 mus musculus
36	67	80.7	433	1 ENOB_RABIT	P25704 oryctolagus cuniculus
37	67	80.7	433	1 ENOB_RAT	P15429 rattus norvegicus
38	67	80.7	433	1 ENOG_HUMAN	P09104 homo sapiens
39	67	80.7	433	1 ENOG_MOUSE	P17183 mus musculus
40	67	80.7	433	1 ENOG_RAT	P07323 rattus norvegicus
41	67	80.7	433	1 ENO_HOMGA	P56252 homarus gammarus
42	67	80.7	433	1 ENO_XENLA	P08734 xenopus laevis
43	67	80.7	433	2 Q8C89	Q6pc89 brachydanio
44	67	80.7	433	2 Q5FH14	Q6th14 brachydanio
45	67	80.7	434	1 ENO_LOLPE	O02654 loligo peale

KW	Glycolysis; Lyase; Mg:magnesium; Multigene family.	SQ	SEQUENCE	433 AA;	PRT;	47145 MW;	B004B965C46R2E0C CRC64;
PT	ACT_SITE 167	Query Match	84.3%	Score 70;	DB 1;	Length 433;	By similarity.
PT	METAL 254	Best Local Similarity	81.2%	Pred. No.	0.00033;	Matches 0;	Magnesium (By similarity).
PT	METAL 308	Matches 13;	Conservative 0;	Mismatches 3;	Indels 0;	Gaps 0;	Magnesium (By similarity).
PT	METAL 336	Matches 14;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;	Magnesium (By similarity).
QY	1 LVNGLCTXQIKTGpac 16	QY	1 LVNGLCTXQIKTGpac 16	SQ	SEQUENCE	433 AA;	47145 MW;
Db	407 LVNGLCTXQIKTGPTC 422	Db	383 LVNGLCTXQIKTGPPC 398	AC	Q9XSJ4;	PRT;	433 AA.
RESULT 2		AC	Q9XSJ4;	PRT;	433 AA.	AC	Q804Y6
ENOA_BOVIN	STANDARD;	DT	16-OCT-2001 (Rel. 40, Last sequence update)	PRT;	88 AA.	ID	Q804Y6
OX	Bovine	DT	05-JUN-2004 (Rel. 44, Last annotation update)	PRT;	88 AA.	ID	Q804Y6
OX	Bos taurus (Bovine).	DE	Alpha_enoate (EC 4.2.2.11) (2-phospho-D-glycerate hydro-lyase) (Non-neuronal enolase) (NNE) (Enolase 1) (Phosphopyruvate hydratase). Name=ENO1;	PRT;	88 AA.	AC	Q804Y6
GN		RN	NCBI_TAXID=9913; [1]	PRT;	88 AA.	ID	Q804Y6
OS	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Buteraria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Odocoileantheria; Bos.	RP	SEQUENCE FROM N.A.	PRT;	88 AA.	AC	Q804Y6
OC		RA	Chapman K.L., Newman B., Hillaby M.C., Freemont A.J., Grant M.E., Boot-Holland R., Wallis G.A.; "Alpha enolase is upregulated in proliferative chondrocytes in the epiphyseal growth plate and in human osteoarthritic tissue.", Submitted (May-1999) to the EMBL/GenBank/DDBJ databases.	PRT;	88 AA.	ID	Q804Y6
OC		RT	-I- CATALYTIC ACTIVITY: 2-phospho-D-glycerate = phosphoenolpyruvate + H(2)O.	PRT;	88 AA.	AC	Q804Y6
CC	-I- COFACTOR: Magnesium is required for catalysis and for stabilizing the dimer (BY similarity).	RL	NON_TER 1	PRT;	88 AA.	ID	Q804Y6
CC	-I- PATHWAY: Glycolysis.	FT	SEQUENCE FROM N.A.	PRT;	88 AA.	AC	Q804Y6
CC	-I- SUBUNIT: Homodimer (BY similarity).	RC	TISSUE=Muscle;	PRT;	88 AA.	ID	Q804Y6
CC	-I- SUBCELLULAR LOCATION: Cytoplasmic (BY similarity).	RA	Kim S., Li P., Zheng X., Dunham R.A., Liu Z.; "Gene expression in the muscles of young and mature channel catfish (Ictalurus punctatus) as analyzed by expressed sequence filters.", Fish Physiol. Biochem. 0:0-0(2003).	PRT;	88 AA.	AC	Q804Y6
CC	-I- TISSUE SPECIFICITY: Three classes of enolase isoenzymes have been identified in mammalian tissues. Isoenzyme alpha is present in most tissues, beta is localized in muscle tissue, and gamma is found only in nervous tissue.	RT	HSSP; PS5252; 1PDZ.	PRT;	88 AA.	ID	Q804Y6
CC	-I- SIMILARITY: Belongs to the enolase family.	DR	GO; GO:0004634; C:phosphopyruvate hydratase complex; IEA.	PRT;	88 AA.	AC	Q804Y6
CC		DR	GO; GO:0006095; P:glycolysis; IEA.	PRT;	88 AA.	ID	Q804Y6
CC		DR	InterPro; IPR000941; Enolase.	PRT;	88 AA.	AC	Q804Y6
CC		DR	Pfam; PF00113; Enolase_C; 1.	PRT;	88 AA.	ID	Q804Y6
CC		DR	ProDom; PD00502; Enolase; 1.	PRT;	88 AA.	AC	Q804Y6
CC		FT	NON_TER 1	PRT;	88 AA.	ID	Q804Y6
CC		FT	SEQUENCE 88 AA; 9830 MW; B014B5B5F0D8B36C1 CRC64;	PRT;	88 AA.	AC	Q804Y6
CC		FT	Query Match 80.7%; Score 67; DB 2; Length 88; Best Local Similarity 81.2%; Pred. No. 0.00027; Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;	PRT;	88 AA.	ID	Q804Y6
CC		QY	1 LVNGLCTXQIKTGpac 16	QY	1 LVNGLCTXQIKTGpac 16	AC	Q9NLPA4
CC		Db	38 LVNGLCTXQIKTGPPC 53	Db	38 LVNGLCTXQIKTGPPC 53	AC	Q9NLPA4
RESULT 4		AC	Q9NLPA4	PRT;	154 AA.	AC	Q9NLPA4;
O9NLPA4	PRELIMINARY;	DT	01-OCT-2000 (TREMBrel. 15, Created)	PRT;	154 AA.	AC	Q9NLPA4;
O9NLPA4		DT	01-OCT-2000 (TREMBrel. 15, Last sequence update)	PRT;	154 AA.	AC	Q9NLPA4;
O9NLPA4		DT	01-MAR-2004 (TREMBrel. 26, Last annotation update)	PRT;	154 AA.	AC	Q9NLPA4;
O9NLPA4		DB	ENO3, muscle enolase 3 beta (Fragment).	PRT;	154 AA.	AC	Q9NLPA4;
O9NLPA4		OS	Homo sapiens (Human).	PRT;	154 AA.	AC	Q9NLPA4;
O9NLPA4		OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Buteraria; Primates; Catarrhini; Hominoidea; Homo.	PRT;	154 AA.	AC	Q9NLPA4;
O9NLPA4		RN	[1]	PRT;	154 AA.	AC	Q9NLPA4;
O9NLPA4		RN	SEQUENCE FROM N.A.	PRT;	154 AA.	AC	Q9NLPA4;
O9NLPA4		RN	Auffray C., Ambrose W., Ballabio A., Estivill X., Gibson K., Lehach H., Pousta K., Lundeberg J.; Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.	PRT;	154 AA.	AC	Q9NLPA4;
O9NLPA4		RN	[2]	PRT;	154 AA.	AC	Q9NLPA4;
O9NLPA4		RN	SEQUENCE FROM N.A.	PRT;	154 AA.	AC	Q9NLPA4;
O9NLPA4		RN	Andreu N., Estivill X., Escarceller M., Sunoy L.; Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.	PRT;	154 AA.	AC	Q9NLPA4;

		Best Local Similarity 81.2%; Pred. No. 0.00046;		Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;	
CC	-!- CATALYTIC ACTIVITY: 2-phospho-D-glycerate = phosphoenolpyruvate + H(2)O.				
CC	-!- COFACTOR: Magnesium is required for catalysis and for stabilizing the dimer (BY SIMILARITY).				
CC	-!- PATHWAY: Glycolysis.				
CC	-!- SUBUNIT: Homodimer (BY SIMILARITY).				
CC	-!- SIMILARITY: Belongs to the enolase family.				
DR	HSSP; P56252; IPI2.				
DR	GO; GO:000015; C:phosphopyruvate hydratase complex; IEA.				
DR	GO; GO:001629; F:lyase activity; IEA.				
DR	GO; GO:000634; F:phosphopyruvate hydratase activity; IEA.				
DR	GO; GO:006096; P:glycolysis; IEA.				
DR	InterPro; IPR000541; Enolase.				
DR	Pfam; PF00113; Enolase C; 1.				
DR	PRINTS; PRO0148; ENOLASE.				
DR	PROSITE; PS00164; ENOLASE; 1.				
FT	NON-TER 1				
SQ	SEQUENCE 159 AA; 17582 MW; 840E266ACD36D3CD CRC64;				
Query Match	80.7%; Score 67; DB 2; Length 159;				
RESULT 5		Best Local Similarity 80.7%; Score 67; DB 2; Length 154;		Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;	
Matches	13;	Best Local Similarity	81.2%;	Pred. No.	0.00045;
Ov	1	1	LWVGLCXQIKTGPC 16		
Db	104	LWVGLCXQIKTGPC 119			
RC	SEQUENCE FROM N.A.				
RC	TISSUE=Ovary;				
RR	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;				
RA	Strauberg R.L., Feingold E.A., Gruber L.H., Derge J.G.,				
RA	Klauner R.D., Collins F.S., Wagner L., Shevchenko C.M., Schuler G.D.,				
RA	Altenschul S.F., Zeeberg B., Bustadt K.H., Schaefer C.F., Bhat N.K.,				
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J.J., Heihs F.,				
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,				
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,				
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,				
RA	Raha S.S., Lognallano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,				
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,				
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Rulyk S.W.,				
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,				
RA	Fahey J., Helton E., Kettteman M., Madan A., Rodrigues S., Sanchez A.,				
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,				
RA	Blakeslee R.W., Touchman J.W., Green E.D., Dickson M.C.,				
RA	Rodriguez A.C., Grimwood J.J., Schmutz J., Myers R.M., Butterfield Y.S.,				
RA	Krzewinski M.I., Skalska U., Smalius D.E., Schnurch A., Schein J.E.,				
RA	Jones S.J., Marx M.A., "Generation and initial analysis of more than 15,000 full-length human				
RT	and mouse cDNA sequences"; RT proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).				
RL	[2]				
RR	SEQUENCE FROM N.A.				
RR	TISSUE=Ovary;				
RA	Strauberg R.; Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.				
RR	-!- CATALYTIC ACTIVITY: 2-phospho-D-glycerate = phosphoenolpyruvate + H(2)O.				
CC	-!- COFACTOR: Magnesium is required for catalysis and for stabilizing the dimer (BY SIMILARITY).				
CC	-!- PATHWAY: Glycolysis.				
CC	-!- SUBUNIT: Homodimer (BY SIMILARITY).				
CC	-!- SIMILARITY: Belongs to the enolase family.				
DR	HSSP; P56252; IPI2.				
DR	GO; GO:000015; C:phosphopyruvate hydratase complex; IEA.				
DR	GO; GO:001629; F:lyase activity; IEA.				
DR	GO; GO:000634; F:phosphopyruvate hydratase activity; IEA.				
DR	GO; GO:006096; P:glycolysis; IEA.				
DR	InterPro; IPR000541; Enolase.				
DR	Pfam; PF00113; Enolase C; 1.				
DR	PRINTS; PRO0148; ENOLASE.				
DR	PROSITE; PS00164; ENOLASE; 1.				
FT	NON-TER 1				
SQ	SEQUENCE 159 AA; 17582 MW; 840E266ACD36D3CD CRC64;				
FT	80.7%; Score 67; DB 2; Length 159;				
RESULT 6		Best Local Similarity 81.2%; Pred. No. 0.00046;		Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;	
QY	1	LWVGLCXQIKTGPC 16			
DR	138 LWVGLCXQIKTGPC 153				
DR	Q96GV1; Q96GV1;				
DR	01-DEC-2001 (TREMBLrel. 19, Created)				
DT	01-MAR-2004 (TREMBLrel. 26, Last sequence update)				
DT	01-MAR-2004 (TREMBLrel. 26, Last annotation update)				
DE	ENOL protein (Fragment).				
GN	Name=ENOL;				
OS	Homo sapiens (Human).				
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Buteraria; Primates; Catarrhini; Hominoidea; Homo.				
OX	NCBI_TaxID=9605;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Ovary;				
RR	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;				
RA	Strauberg R.L., Feingold E.A., Gruber L.H., Derge J.G.,				
RA	Klauner R.D., Collins F.S., Wagner L., Shevchenko C.M., Schuler G.D.,				
RA	Altschul S.F., Zeeberg B., Bustadt K.H., Schaefer C.F., Bhat N.K.,				
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J.J., Heihs F.,				
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,				
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,				
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,				
RA	Raha S.S., Lognallano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,				
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,				
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Rulyk S.W.,				
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,				
RA	Fahey J., Helton E., Kettteman M., Madan A., Rodrigues S., Sanchez A.,				
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,				
RA	Blakeslee R.W., Touchman J.W., Green E.D., Dickson M.C.,				
RA	Rodriguez A.C., Grimwood J.J., Schmutz J., Myers R.M., Butterfield Y.S.,				
RA	Krzewinski M.I., Skalska U., Smalius D.E., Schnurch A., Schein J.E.,				
RA	Jones S.J., Marx M.A., "Generation and initial analysis of more than 15,000 full-length human				
RT	and mouse cDNA sequences"; RT proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).				
RL	[2]				
RR	SEQUENCE FROM N.A.				
RR	TISSUE=Ovary;				
RA	Strauberg R.; Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.				
RR	-!- CATALYTIC ACTIVITY: 2-phospho-D-glycerate = phosphoenolpyruvate + H(2)O.				
CC	-!- COFACTOR: Magnesium is required for catalysis and for stabilizing the dimer (BY SIMILARITY).				
CC	-!- PATHWAY: Glycolysis.				
CC	-!- SUBUNIT: Homodimer (BY SIMILARITY).				
CC	-!- SIMILARITY: Belongs to the enolase family.				
DR	HSSP; P56252; IPI2.				
DR	GO; GO:000015; C:phosphopyruvate hydratase complex; IEA.				
DR	GO; GO:001629; F:lyase activity; IEA.				
DR	GO; GO:000634; F:phosphopyruvate hydratase activity; IEA.				
DR	GO; GO:006096; P:glycolysis; IEA.				
DR	InterPro; IPR000541; Enolase.				
DR	Pfam; PF00113; Enolase C; 1.				
DR	PRINTS; PRO0148; ENOLASE.				
DR	PROSITE; PS00164; ENOLASE; 1.				
FT	NON-TER 1				
SQ	SEQUENCE 159 AA; 17582 MW; 840E266ACD36D3CD CRC64;				
FT	80.7%; Score 67; DB 2; Length 159;				

Query Match 80.7%; Score 67; DB 2; Length 184;
 Best Local Similarity 81.2%; Pred. No. 0.00053; 0; Mismatches 3; Indels 0; Gaps 0;

Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

RESULT 7
 Q7ZMS5 PRELIMINARY; PRT; 259 AA.
 ID Q7ZMS5; PRELIMINARY; PRT; 259 AA.
 AC Q7ZMS5; PRELIMINARY; PRT; 259 AA.
 DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DR Enolase (Fragment).
 OS Sparus aurata (Giltthead sea bream).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 RA Diatchenko L., Marnusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Ronald M.P., Casavant T.L., Scheetz T.B., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Lognallano N.A., Peters G.J., Abramson C.M., Schuler G.D., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muñoz D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopercyigii; Teleostei; Butelostomii; Acanthomorpha; Acanthopterygii; Percormorpha; Perciformes; Percoidei; Sparidae; Sparus.
 NCBI_TaxID=9606; [1]
 OX — TAXID=8175;
 RN [1] —
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Ribas L., Mackenzi S., Planas J., Monetti C., Bernardini G., Tort L.; Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
 RL CC -I CATALYTIC ACTIVITY: 2-phospho-D-glycerate = phosphoenolpyruvate + H(2)O.
 CC -I COFACTOR: Magnesium is required for catalysis and for stabilizing the dimer (By similarity).
 CC -I PATHWAY: Glycolysis.
 CC -I SUBUNIT: Homodimer (By similarity).
 CC -I SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -I SIMILARITY: Belongs to the enolase family.
 DR EMBL: AY263379; AAO92646.1; —.
 DR HSSP: P5652; 1PDZ.
 DR GO; GO:000015; C:phosphopyruvate hydratase complex; IEA.
 DR GO; GO:0016829; F:lyase activity; IEA.
 DR GO; GO:000287; F:magnesium ion binding; IEA.
 DR GO; GO:004634; F:phosphopyruvate hydratase activity; IEA.
 DR GO; GO:000096; P:glycolysis; IEA.
 DR InterPro: IPR00941; Enolase.
 DR Pfam: PF00113; Enolase_C; 1.
 DR PRINTS; PRO0148; ENOLSE.
 DR ProDom; PD000902; Enolase; 1.
 DR PROSITE; PS00164; ENOLASE; 1.
 KW Glycolysis; Lyase; Magnesium.
 FT NON-TER 1 259 259 AA; 28484 MW; 1DE915D38955331B CRC64;
 SQ SEQUENCE 259 AA; 28484 MW; 1DE915D38955331B CRC64;
 Query Match 80.7%; Score 67; DB 2; Length 259;
 Best Local Similarity 81.2%; Pred. No. 0.00074; 0; Mismatches 3; Indels 0; Gaps 0;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

RESULT 8
 Q8WUT1 PRELIMINARY; PRT; 264 AA.
 ID Q8WUT1; PRELIMINARY; PRT; 264 AA.
 AC Q8WUT1; PRELIMINARY; PRT; 264 AA.
 DT 01-MAR-2002 (TREMBLrel. 20, Created)
 DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DR ENOL Protein (Fragment).
 GN Name=ENOL;
 OS Homo sapiens (Human).

RESULT 9
 Q9BT62 PRELIMINARY; PRT; 272 AA.
 ID Q9BT62; PRELIMINARY; PRT; 272 AA.
 AC Q9BT62; PRELIMINARY; PRT; 272 AA.
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE ENOL Protein (Fragment).
 GN Name=ENOL;
 OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OC NCBI_TaxID=9606;
 [1]

RN SEQUENCE FROM N.A.

RC TISSUE-Placenta;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,
 Klausner R.D., Collins F.S., Wagner L., Shemesh C.M., Schuler G.D.,
 Altshul S.F., Zeeberg B., Buetow K.H.,
 Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heleb F.,
 Blatchenko L., Minuska K., Farmer A.A., Rubin G.M., Hong L.,
 Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
 Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 Raha S., Loqueland N.A., Peters G.J., Abramson R.D., Mulally S.J.,
 Bosak S.A., McEwan P.J., McKernan J.J., Malek J.A., Gunaratne P.H.,
 Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 Villalon D.K., Muñiz D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 Fahy J., Heaton E., Ketteman M., Madan A., Rodriguez S., Sanchez A.,
 Whiting M., Madan A., Young A.C., Shvchenko Y., Bouffard G.G.,
 Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 Rodriguez A.C., Grimm J., Schmitz R.M., Butterfield Y.S.,
 Krywinski M.I., Skalska U., Smilus D.E., Schnurch A., Schein J.B.,
 Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15, 000 full-length human
 RT and mouse cDNA sequences",
 RT proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RL [2]

RN SEQUENCE FROM N.A.

RC TISSUE-Placenta;

RA Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.

-I CATALYTIC ACTIVITY: 2-phospho-D-glycerate = phosphoenolpyruvate +
 H(2)O.

-I COFACTOR: Magnesium is required for catalysis and for stabilizing
 the dimer (By similarity).

-I PATHWAY: Glycolysis.

-I SUBUNIT: Homodimer (By similarity).

-I SUBCELLULAR LOCATION: Cytoplasmic (By similarity).

CC -I SIMILARITY: Belongs to the enolase family.

DR BC004325; AAH04325.1; -.

CC HSPB_P5625; 1PZ.

DR GO:0000015; C:phosphopyruvate hydratase complex; IEA.

CC GO:0011629; P:lyase activity; IEA.

CC GO:0000287; P:magnesium ion binding; IEA.

CC GO:0004634; P:phosphopyruvate hydratase activity; IEA.

DR EMBL: BC004325; AAH04325.1; -.

DR HSPB_P5625; 1PZ.

DR GO:0000015; C:phosphopyruvate hydratase complex; IEA.

DR GO:0011629; P:lyase activity; IEA.

DR GO:0000287; P:magnesium ion binding; IEA.

DR GO:0004634; P:phosphopyruvate hydratase activity; IEA.

DR InterPro: IPR000941; Enolase.

DR Pfam: PF00113; Enolase_C; 1.

DR Pfam: PF0352; Enolase_N; 1.

DR PRINTS: PR00148; ENOLASE.

DR PRODOM: PD000902; ENOLASE; 1.

DR PROSITE: PS00164; ENOLASE; 1.

DR InterPro: IPR000941; Enolase.

DR Pfam: PF00113; Enolase_C; 1.

DR GO:0000015; C:phosphopyruvate hydratase complex; IEA.

DR GO:0011629; P:lyase activity; IEA.

DR GO:0000287; P:magnesium ion binding; IEA.

DR GO:0004634; P:phosphopyruvate hydratase activity; IEA.

DR InterPro: IPR000941; Enolase.

DR Pfam: PF00113; Enolase_C; 1.

DR Pfam: PF0352; Enolase_N; 1.

DR PRINTS: PR00148; ENOLASE.

DR PRODOM: PD000902; ENOLASE; 1.

DR PROSITE: PS00164; ENOLASE; 1.

KW Glycolysis; Lyase; Magnesium.

FT NON_TER 1 1

SQ SEQUENCE 336 AA; 36308 MW; 2C295B0A28F19301 CRC64;

Query Match 80.7%; Score 67; DB 2; Length 336;
 Best Local Similarity 81.2%; Pred. No. 0.00092; Mismatches 0; Indels 0; Gaps 0;

Matches 13; Conservative 0; Misnatches 3; Indels 0; Gaps 0;

QY 1 LVVGLCTQIKTGAPC 16

Db 286 LVVGLCTQIKTGAPC 301

RESULT 11

Q922A0 PRELIMINARY; PRT; 336 AA.

ID Q922A0 PRELIMINARY; PRT; 336 AA.

AC Q922A0; Created)

DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)

DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)

DE Eno2 protein (Fragment).

GN Name=sno2;

OS Mus musculus (Mouse).

OC Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OC NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-FVB/N; TISSUE-Mammary tumor. C3;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,
 Klausner R.D., Colling F.S., Wagner L., Shemesh C.M., Schuler G.D.,
 Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Alpha enolase (Fragment).

RESULT 10

Q71V37 PRELIMINARY; PRT; 336 AA.

Query Match 80.7%; Score 67; DB 2; Length 272;
 Best Local Similarity 81.2%; Pred. No. 0.00076; Mismatches 3; Indels 0; Gaps 0;

Matches 13; Conservative 0; Misnatches 3; Indels 0; Gaps 0;

QY 1 LVVGLCTQIKTGAPC 16

Db 222 LVVGLCTQIKTGAPC 237

RA Hopkins R.F., Jordan H., Moore T., Max S.J., Wang J., Heihs F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Brownstein M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Schatz T.E.,
 RA Bosak S.A., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzyk D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahay J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Malek J.A., Gunaratne P.H.,
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnurch A., Schein J.E.,
 RA Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15, 000 full-length human
 RT and mouse cDNA sequences"; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FB/B; TISSUE=Mammary tumor. C3;
 RL Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
 CC -!- CATALYTIC ACTIVITY: 2-phospho-D-glycerate = phosphoenolpyruvate +
 H(2)O.
 CC -!- COFACTOR: Magnesium is required for catalysis and for stabilizing
 the dimer (By similarity).
 CC -!- PATHWAY: Glycolysis.
 CC -!- SUBUNIT: Homodimer (By similarity).
 CC -!- SUBCELLULAR LOCATION: Cyttoplasmic (By similarity).
 CC -!- SIMILARITY: Belongs to the enolase family.
 DR EMBL: BC005018; AAH05018.1; -.
 DR HSSP: P56257; 1PDZ.
 DR MGD: MGI:93394; Bn02.
 DR GO: GO:0000105; C:phosphopyruvate hydratase complex; IBA.
 DR GO: GO:0016829; P:lyase activity; IBA.
 DR GO: GO:0000287; F:magnesium ion binding; IBA.
 DR GO: GO:0004634; F:phosphopyruvate hydratase activity; IBA.
 DR GO: GO:0006096; P:glycolysis; IBA.
 DR Pfam: PF00113; Enolase_C; 1.
 DR ProDom: PDD00902; Enolase_1.
 DR PROSITE: PS00164; ENOLASE; 1.
 DR KW GLYCOLYSIS; Lyase; Magnesium.
 DR NON_TER 1
 SQ SBQENCE 338 AA; 37146 MW; B0F2F321D7749484 CRC64;

Query Match 80.7%; Score 67; DB 2; Length 338;
 Best Local Similarity 81.2%; Pred. No. 0.00092; Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 LVVGLCTQIKTGPC 16
 Db 288 LVVGLCTQIKTGPC 303

RESULT 12

O6GMP2 PRELIMINARY; PRT; 341 AA.

ID O6GMP2; PRELIMINARY; PRT; 341 AA.

AC 06GMP2; PRELIMINARY; PRT; 341 AA.

DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)

DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)

DE ENO1 protein.

GN Name=ENO1;

OS Homo Sapiens (Human)

OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

NCBI_TaxID=9606; [1]

RN SEQUENCE FROM N.A.

RC TISSUE=Pancreas;

RA MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA

Klauser R.D., Collins F.S., Wagner L., Sheppard C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaeffer C.F., Bhattacharjee A.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.J., Wang J., Heihs F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Brownstein M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Schatz T.E.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schatz T.E.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzyk D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahay J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Malek J.A., Gunaratne P.H.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzyk D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahay J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmitz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnurch A., Schein J.E.,
 RA Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15, 000 full-length human
 RT and mouse cDNA sequences"; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FB/B; TISSUE=Mammary tumor. C3;
 RL Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
 CC -!- CATALYTIC ACTIVITY: 2-phospho-D-glycerate = phosphoenolpyruvate +
 H(2)O.
 CC -!- COFACTOR: Magnesium is required for catalysis and for stabilizing
 the dimer (By similarity).
 CC -!- PATHWAY: Glycolysis.
 CC -!- SUBUNIT: Homodimer (By similarity).
 CC -!- SIMILARITY: Belongs to the enolase family.
 DR EMBL: BC073991; AAH73991.1; -.
 DR GO: GO:0000105; C:phosphopyruvate hydratase complex; IBA.
 DR GO: GO:0016829; F:lyase activity; IBA.
 DR GO: GO:0000287; F:magnesium ion binding; IBA.
 DR GO: GO:0004634; F:phosphopyruvate hydratase activity; IBA.
 DR GO: GO:0006096; P:glycolysis; IBA.
 DR InterPro: IPR000941; Enolase.
 DR Pfam: PF00113; Enolase_C; 1.
 DR Pfam: PF03952; Enolase_N; 1.
 DR PRINTS: PR00148; ENOLASE.
 DR ProDom: PDD00902; Enolase; 1.
 DR PROSITE: PS00164; ENOLASE; 1.
 DR KW GLYCOLYSIS; Lyase; Magnesium.
 DR NON_TER 1
 SQ SBQENCE 341 AA; 36928 MW; 96D437CF21772928 CRC64;

Query Match 80.7%; Score 67; DB 2; Length 341;
 Best Local Similarity 81.2%; Pred. No. 0.00093; Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 LVVGLCTQIKTGPC 16
 Db 291 LVVGLCTQIKTGPC 306

RESULT 13

O99KRT7 PRELIMINARY; PRT; 353 AA.

ID O99KRT7 PRELIMINARY; PRT; 353 AA.

AC 099KRT7; PRELIMINARY; PRT; 353 AA.

DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)

DE Enol protein (Fragment).

GN Name=ENO1;

OS Mus musculus (Mouse).

OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Buteraria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

NCBI_TaxID=10090; [1]

RN SEQUENCE FROM N.A.

RC TISSUE=Pancreas;

RA MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA

DR EMBL; AL833741; CHH56247.1; -.
KW HYPothetical protein.
FT 1
NON_TER
SQ 374 AA; 40512 MW; 681A021EB75C43D9 CRC64;
Query Match 80.7%; Score 67; DB 2; Length 374;
Best Local Similarity 81.2%; PRed. No. 0.001; Mismatches 3; Indels 0; Gaps 0;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 LVNGLCRQKINGPAC 16
Db 324 LVNGLCRQKINGPAC 339

Search completed: July 13, 2005, 12:13:15
Job time : 58 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 13, 2005, 12:06:24 ; Search time 38 Seconds

(without alignments)

4.3.044 Million cell updates/sec

Title: US-09-647-457E-1
Perfect score: 83
Sequence: 1 LVVGLCTXQIKTGPACKX 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched:

283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : PIR_79;*

 1: pir1;*
 2: pir2;*
 3: pir3;*
 4: pir4;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ALIGNMENTS

RESULT	1
I37360	phosphopyruvate hydratase (EC 4.2.1.11), lung - human
N	Alternate name: enolase
C;Species:	Homo sapiens (man)
C;Date:	21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 09-Jul-2004
C;Accession:	I37360; S22071
R;Verma, M.; Kurl, R.N.	
Biochem. Int. 30, 293-303, 1993	
A;Title:	Human lung enolase: cloning and sequencing of cDNA and its inducibility with d
A;Reference number:	I37360
A;Function:	
A;Description:	catalyzes the reversible dehydration of 2-phospho-D-glyceric acid to phosphoglycerate
A;Molecule type:	mRNA
A;Residues:	1-458 <HTR>
A;Cross-references:	UNIPROT:Q05524; EMBL:X66610; NID:931178; PIDN:CAA47179.1; PID:93117
A;Note:	submitted to the EMBL Data Library, June 1992
C;Function:	
A;Description:	preliminary; translated from GB/EMBL/DDBJ
A;Pathway:	gluconeogenesis; glycolysis
C;Superfamily:	enolase
C;Keywords:	carbon-oxygen lyase; gluconeogenesis; glycolysis; hydro-lyase; magnesium
F;43;Binding site:	magnesium 2 (Ser) #status predicted
P;219,364/Active site:	Glu, Lys #status Predicted
P;254,308,336/Binding site:	magnesium 1 (Asp, Glu, Asp) #status predicted
Query Match	91.6%; Score 76; DB 2; Length 458;
Best Local Similarity	87.5%; Pred. No. 1.2e-05;
Matches	14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY	1 LVVGLCTXQIKTGAC 16
DB	407 LVVGLCTXQIKTGAC 422

RESULT 2

150026	phosphopyruvate hydratase (EC 4.2.1.11) alpha - American alligator (fragment)
N	Alternate names: alpha-enolase
C;Species:	Alligator mississippiensis (American alligator)
C;Date:	21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 09-Jul-2004
C;Accession:	I50026
R;Hedges, S.B.	
Proc. Natl. Acad. Sci. U.S.A. 91, 2621-2624, 1994	
A;Title:	Molecular evidence for the origin of birds.
A;Reference number:	A53470; MJD:94195794; PMID:8146164
A;Accession:	I50026
A;Status:	Preliminary; nucleic acid sequence not shown; translation not shown; translate
A;Molecule type:	mRNA
A;Residues:	1-395 <HTR>
A;Cross-references:	UNIPROT:P42897; GB:L28078; NID:9472795; PID:AA53671.1; PID:9472797
C;Superfamily:	enolase

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C;Keywords: carbon-oxygen lyase; hydro-lyase
Query Match 80.7%; Score 67; DB 2; Length 395;
Best Local Similarity 81.2%; Pred. No. 0.00041; Mismatches 0; Indels 0; Gaps 0;
Matches 13; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Qy 1 LNVGLCTXQIKTGAPC 16
Db 362 LNVGLCTQIKTGAPC 377

RESULT 3

A37210
phosphopyruvate hydratase (EC 4.2.1.11) beta - rabbit
N;Alternate name: enolase beta
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 16-Aug-2004
C;Accession: A37210
A;Status: preliminary
R;Chin, C.C.O.
J. Protein Chem. 9, 427-432, 1990
A;Title: The primary structure of rabbit muscle enolase.
A;Reference number: A37210; MUID:9113295; PMID:2275753
A;Accession: A37210
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-433 <CHI>
A;Cross-references: UNIPROT:P25704
C;Superfamily: Enolase
C;Keywords: acetylated amino end; carbon-oxygen lyase; hydro-lyase
F;1/Modified site: acetylated amino end (Ala) #status experimental

Query Match 80.7%; Score 67; DB 2; Length 433;
Best Local Similarity 81.2%; Pred. No. 0.00045; Mismatches 0; Indels 0; Gaps 0;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LNVGLCTXQIKTGAPC 16
Db 383 LNVGLCTQIKTGAPC 398

RESULT 4

N0HUG
phosphopyruvate hydratase (EC 4.2.1.11) gamma - human
N;Alternate names: enolase gamma; neuron-specific enolase
C;Species: Homo sapiens (man)
C;Date: 31-Mar-1990 #sequence revision 31-Mar-1990 #text_change 16-Aug-2004
C;Accession: JU0060; S16163; S02077; I15659; S02616; S88303
R;Olika, D.; Barba, G.; Barbieri, G.; Giallongo, A.; Feo, S.
Gene 79, 355-360, 1989
A;Title: Cloning, expression and sequence homologies of cDNA for human gamma enolase.
A;Reference number: JU0060; MUID:90006764; PMID:2792767
A;Accession: JU0060
A;Molecule type: mRNA
A;Residues: 1-434 <OL1>
A;Cross-references: UNIPROT:P03104; GB:MA22349; NID:9951199; PIDN:AAB59554.1; PID:gi82116
R;Oliva, D.; Cali, L.; Feo, S.; Giallongo, A.
Genomics 10, 157-165, 1991
A;Title: Complete structure of the human gene encoding neuron-specific enolase.
A;Reference number: S16163; MUID:91257823; PMID:2045099
A;Accession: S16163
A;Molecule type: DNA
A;Residues: 1-434 <OL2>
A;Cross-references: GB:X51956; NID:931164; PIDN:CAA36215.1; PID:gi31165
R;McAlleese, S.M.; Dunbar, B.; Pothbergill, J.E.; Hinks, L.J.; Day, I.N.M.
Bur. J. Biochem. 178, 413-417, 1988
A;Title: Complete amino acid sequence of the neurone-specific gamma isozyme of enolase
A;Reference number: S02077; MUID:89091176; PMID:3208766
A;Accession: S02077
A;Molecule type: mRNA
A;Residues: 2-33 'O' 5-23 'M' 241-434 <MC>
A;Cross-references: EMBL:X13120; NID:931145; PIDN:CAA31512.1; PID:gi930063
A;Note: part of this sequence was confirmed by protein sequencing
A;Note: 264-Ala and 395-Ala were also found

R;Van Obberghen, E.; Kamholz, J.; Bishop, J.G.
J. Neurosci. Res. 19, 450-456, 1988
A;Title: Human gamma enolase: isolation of a cDNA clone and expression in normal and tumor cells
A;Reference number: 156569; MUID:88259288; PMID:3385803
A;Accession: 156569
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 'GC', 29-126, 'N', 128-434 <VAN>
A;Cross-references: GB:M36768; NID:gi182117; PIDN:AAA52388.1; PID:gi182118
R;Day, I.N.M.; Allsopp, M.T.E.P.; Moore, D.C.M.; Thompson, R.J.
FEBS Lett. 222, 139-143, 1987
A;Title: Sequence conservation in the 3'-untranslated regions of neurone-specific enolases
A;Reference number: S02616; MUID:88005129; PMID:3653393
A;Accession: S02616
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 425-434 <DAY>
A;Cross-references: GB:Y00691; GB:M27610
R;Harrington, C.R.; Quinn, G.B.; Hurt, J.; Day, I.N.M.; Waschik, C.M.
Blochim. Biophys. Acta 1158, 120-128, 1993
A;Title: Characterisation of an epitope specific to the neuron-specific isoform of human beta/44-protein
A;Reference number: S38303; MUID:94002176; PMID:7691181
A;Accession: S38303
A;Molecule type: protein
A;Residues: 156-173 <HAR>
A;Map position: 12p13-12p13
A;Introns: 29/1, 61/1; 80/3; 104/1; 148/3; 223/1; 289/1; 356/2; 392/2; 412/2
C;Complex: homodimer
C;Function:
A;Description: catalyzes the reversible dehydration of 2-phospho-D-glyceric acid to phosphoglycerate
A;Pathway: gluconeogenesis; glycolysis
C;Superfamily: Enolase
C;Keywords: blocked amino end; brain; carbon-oxygen lyase; gluconeogenesis; glycolysis;
F;2-434/Product: phosphopyruvate hydratase gamma #status predicted <MAT>
F;2/Modified site: blocked amino end (Ser) (in mature form) (probably acetylated) #status predicted
F;2/Binding site: magnesium 2 (Ser) #status predicted
F;210, 343/Active site: Glu, Lys #status predicted
F;245, 293, 318/Binding site: magnesium 1 (Asp, Glu, Asp) #status predicted
Query Match 80.7%; Score 67; DB 1; Length 434;
Best Local Similarity 81.2%; Pred. No. 0.00045; Mismatches 0; Indels 0; Gaps 0;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LNVGLCTXQIKTGAPC 16
Db 384 LNVGLCTQIKTGAPC 399

RESULT 5

N0MSB
phosphopyruvate hydratase (EC 4.2.1.11) beta - mouse
N;Alternate names: enolase beta
C;Species: Mus musculus (house mouse)
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Aug-2004
C;Accession: S17109; S10036; S29675; A33921
C;Accession: S17109; S10036; S29675; A33921
R;Lamande, N.; Brosset, S.; Keller, A.; Lucas, M.; Lazar, M.
submitted to the EMBL Data Library, September 1991
A;Reference number: S17109
A;Accession: S17109
A;Molecule type: DNA
A;Residues: 1-434 <LM>
A;Cross-references: UNIPROT:P21550; EMBL:X61600; NID:950848; PIDN:CAA43797.1; PID:gi50849
R;Peterson, C.A.; Cho, M.; Rastinejad, F.; Blau, H.M.
submitted to the EMBL Data Library, October 1991
A;Description: Beta-enolase: a gene expressed in undifferentiated postnatal myoblasts th
A;Reference number: S18036
A;Accession: S18036

	Db	384 LVVGLCTQIKTGAPC 399
A;Molecule type: mRNA		
A;Residues: I-1434 <P>ET>		
A;Cross-references: EMBL:X62667; NID:950143; PIDN:CAA44540.1; PID:950144		
R;Lazar, M.; Lamande, N.; Brosset, S.; Lucas, M.; Keller, A.		
submitted to the EMBL Data Library, February 1991		
A;Reference number: S29675		
A;Accession: S29675		
A;Status: preliminary		
A;Molecule type: mRNA		
A;Cross-references: EMBL:X57747; NID:950846; PIDN:CAA40913.1; PID:950847		
R;Lamande, N.; Mazo, A.M.; Lucas, M.; Montarras, D.; Pinset, C.; Giro, P.; Legault-Demar		
proc. Natl. Acad. Sci. U.S.A. 86, 4455-4459, 1989		
A;Title: Murine muscle-specific enolase: cDNA cloning, sequence, and developmental expre		
ss. Proc. Natl. Acad. Sci. U.S.A. 86, 4455-4459, 1989		
A;Reference number: A33921		
A;Accession: A33921		
A;Status: preliminary		
A;Molecule type: mRNA		
A;Residues: 59-233, 'NA', 236-434 <LLA2>		
A;Cross-references: GB: M20745; NID:9193029; PIDN:AAA37554.1; PID:9387144		
A;Experimental source: skeletal muscle		
C;Genetics:		
A;Introns: 29/1; 61/1; 80/3; 104/1; 148/3; 223/1; 289/1; 356/2; 392/3; 412/2		
A;Function:		
A;Description: catalyzes the reversible dehydration of 2-phospho-D-glyceric acid to phos		
C;Pathway: gluconeogenesis; glycolysis		
C;Superfamily: Enolase		
C;Keywords: carbon-carbon lyase; carbon-oxygen lyase; dimer; gluconeogenesis; glycolysis		
F;40/Binding site: magnesium 2 (Ser) #status predicted		
F;21/345/act1/e site: Glu, Lys #status predicted		
F;245,293,318/Binding site: magnesium 1 (Asp, Glu, Asp) #status predicted		
Query Match		
Best Local Similarity		80.7%
Matches		13;
Qy		Conservative
Oy		0;
Db		Mismatches 3;
Matchs		Indels 0;
Gaps		0;
RESULT 6		
NOXL		
phosphopyruvate hydratase (EC 4.2.1.11) ENO1 - African clawed frog		
N;Alternate names: enolase ENO1		
C;Species: Xenopus laevis (African clawed frog)		
C;Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 16-Aug-2004		
C;Accession: S00463		
R;Segil, N.; Shrutiowski, A.; Dworkin, M.B.; Dworkin-Rastl, B.		
Biochem. J. 251, 31-39, 1988		
A;Title: Enolase isoenzymes in adult and developing Xenopus laevis and characterization		
A;Reference number: S00463; MUID:88268812; PMID:3390159		
A;Accession: S00463		
A;Molecule type: mRNA		
A;Residues: 1-1434 <SEQ>		
A;Cross-references: UNIPROT:P08734; EMBL:Y00718; NID:946679; PIDN:CAA68706.1; PID:954680		
C;Genetics:		
A;Gene: ENOL		
C;Function:		
A;Description: catalyzes the reversible dehydration of 2-phospho-D-glyceric acid to phos		
A;Pathway: gluconeogenesis; glycolysis		
C;Superfamily: Enolase		
C;Keywords: carbon-oxygen lyase; dimer; gluconeogenesis; glycolysis; hydro-lyase; magne		
F;21/0/343/Active site: Glu, Lys #status predicted		
F;245,293,318/Binding site: magnesium 1 (Asp, Glu, Asp) #status predicted		
Query Match		
Best Local Similarity		80.7%;
Matches		13;
Qy		Conservative
Oy		0;
Db		Mismatches 3;
Matchs		Indels 0;
Gaps		0;
RESULT 7		
JCL039		
phosphopyruvate hydratase (EC 4.2.1.11) - rat		
N;Alternate name: neuron-specific enolase		
C;Species: Rattus norvegicus (Norway rat)		
C;Date: 05-Mar-1993 #sequence_revision 19-Oct-1995 #text_change 03-May-1996		
R;Zhao, C.; Wang, L.B.; Song, X.W.; Zhang, J.Y.		
Chinese Biochem. J. 10, 270-277, 1994		
A;Title: cDNA cloning and sequencing of the NSB gene from rat brain.		
A;Reference number: JCL039		
A;Accession: JCL039		
A;Molecule type: mRNA		
A;Residues: 1-134 <ZER>		
A;Experimental source: brain, Wistar		
C;Comment: This enzyme is a specific marker protein for the development of nervous syste		
C;Genetics:		
A;Gene: ns ³		
A;Superfamily: enolase		
C;Keywords: brain; carbon-oxygen lyase; hydro-lyase		
Query Match		
Best Local Similarity		80.7%;
Matches		13;
Qy		Conservative
Oy		0;
Db		Mismatches 3;
Matchs		Indels 0;
Gaps		0;
RESULT 8		
JCL4186		
phosphopyruvate hydratase (EC 4.2.1.11) alpha chain - chicken		
N;Alternate names: alpha-2-phospho-D-glycerate hydrolase; enolase		
C;Species: Gallus gallus (chicken)		
C;Date: 10-Sep-1995 #sequence_revision 27-Oct-1995 #text_change 09-Jul-2004		
C;Accession: JCL4186		
R;Tanaka, M.; Maeda, K.; Nakashima, K.		
J; Biochem. 117, 554-559, 1995		
A;Title: Chicken alpha-2-enolase but not beta-enolase has a Src-dependent tyrosine-phospho		
A;Reference number: JCL4186; MUID:9535305; PMID:7629021		
A;Accession: JCL4186		
A;Molecule type: mRNA		
A;Residues: 1-1434 <TPR>		
A;Cross-references: UNIPROT:P51913; DDSD:D37900; NID:974175; PIDN:BA007132.1; PID:9741		
A;Experimental source: brain		
C;Comment: This is a glycolytic enzyme and multiple isoenzyme forms were reported which		
C;Keywords: carbon-oxygen lyase; hydro-lyase; phosphoprotein		
C;Superfamily: enolase		
F;44/Binding site: phosphate (Tyr) (covalent) #status predicted		
Query Match		
Best Local Similarity		80.7%;
Matches		13;
Qy		Conservative
Oy		0;
Db		Mismatches 3;
Matchs		Indels 0;
Gaps		0;
RESULT 9		
JCL4187		
phosphopyruvate hydratase (EC 4.2.1.11) beta chain - chicken		
N;Alternate names: beta-2-phospho-D-glycerate hydrolase; enolase		
C;Species: Gallus gallus (chicken)		
C;Date: 14-Sep-1995 #sequence_revision 27-Oct-1995 #text_change 09-Jul-2004		
C;Accession: JCL4187		
R;Tanaka, M.; Maeda, K.; Nakashima, K.		
J; Biochem. 117, 554-559, 1995		

A;Title: Chicken alpha-enolase but not beta-enolase has a Src-dependent tyrosine-phospho
A;Reference number: JC4186; MUID:95355305; PMID:7629021
A;Molecule type: mRNA
A;Residues: 1-1434 <TAN>
A;Cross-references: UNIPROT:P07322; DDBJ:D37901; NID:9374177; PIDN:BA07133.1; PID:g1616
C;Comment: This is a glycolytic enzyme and multiple isoenzyme forms were reported which
rates for tyrosine phosphorylation in Rous sarcoma virus and is important in all the emb
C;Superfamily: enolase
C;Keywords: acetylated amino end; carbon-oxygen lyase; hydro-lyase; phosphoprotein
P/I;Modified site: acetylated amino end (Met) #status: experimental

Query Match 80.7%; Score 67; DB 2; Length 434;
Best Local Similarity 81.2%; Pred. No. 0.00045;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 LWVGCTXQIKTGAPC 16
Db 384 LWVGCTQIKTGAPC 399

RESULT 10

S06756
phosphopyruvate hydratase (EC 4.2.1.11) beta - human
N;Alternate names: enolase beta; enolase, skeletal muscle; phosphopyrivate hydratase, mi
C;Species: Homo sapiens (man)
C;Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 09-Jul-2004
C;Accession: S06756; S14759; S59333; S33330; S08685; S31650
R;Peshavaria, M.; Hinks, L.J.; Day, I.N.M.
Nucleic Acids Res. 17, 882, 1989
A;Title: Structure of human muscle (beta) enolase mRNA and protein deduced from a genomic
A;Reference number: S06756; MUID:90067857; PMID:2587223
A;Accession: S06756
A;Molecule type: mRNA
A;Residues: 1-434 <PE3>
A;Cross-references: UNIPROT:PI3929; EMBL:X1604; NID:931169; PIDN:CAA34513.1; PID:g31170
R;Peshavaria, M.; Day, I.N.M.
Bloch, J. 275, 427-433, 1991
A;Title: Molecular structure of the human muscle-specific enolase gene (ENO3).
A;Reference number: S14759; MUID:91222137; PMID:1840492
A;Accession: S14759
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-34 <PE2>
A;Cross-references: EMBL:X55976
R;Calli, L.; Feo, S.; Oliva, D.; Gaillongo, A.
Nucleic Acids Res. 18, 1893, 1990
A;Title: Nucleotide sequence of a cDNA encoding the human muscle-specific enolase (MSB).
A;Reference number: S15933; MUID:90245587; PMID:2236365
A;Accession: S15933
A;Molecule type: mRNA
A;Residues: 1-34 'A' 86-161 'K' 163-434 <CAL>
A;Cross references: EMBL:X51937; NID:931788; PIDN:CAA36216.1; PID:g34789
R;Gaillongo, A.; Venturelli, S.; Oliva, D.; Barbieri, G.; Rubino, P.; Feo, S.
Bur. J. Biochem. 214, 367-374, 1993
A;Title: Structural features of the human gene for muscle-specific enolase. Differential
A;Reference number: S33330; MUID:93292497; PMID:8513787
A;Accession: S33330
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-161 'K' 163-434 <GIA>
A;Cross-references: EMBL:X56822; NID:931166; PIDN:CAA40163.1; PID:g31167
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1990
A;Gene: GDB:EN03
A;Cross-references: GDB:119873; OMIM:131370
A;Map position: 17pter-17p12
A;Introns: 29/1; 6/1; 8/3; 104/1; 148/3; 223/1; 289/1; 356/2; 392/3; 412/2
C;Superfamily: enolase
C;Keywords: carbon-oxygen lyase; gluconeogenesis; glycolysis; hydro-lyase; muscle; skele

Query Match 80.7%; Score 67; DB 2; Length 434;
Best Local Similarity 81.2%; Pred. No. 0.00045;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 LWVGCTXQIKTGAPC 16
Db 384 LWVGCTQIKTGAPC 399

RESULT 11

S10246
phosphopyruvate hydratase (EC 4.2.1.11) alpha - mouse
N;Alternate names: 2-phosphoglycerate dehydratase; enolase alpha
C;Species: Mus musculus (house mouse)
C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 09-Jul-2004
C;Accession: S10246; A56781
R;Kachadurian, M.; Dumont, X.; Chalon, P.; Lelias, J.M.; Lamande, N.; Lucas, M.; Lazar, M.; C
Nucleic Acids Res. 18, 3638, 1990
A;Title: Nucleotide sequences of cDNAs alpha and gamma enolase mRNAs from mouse brain.
A;Reference number: S10246; MUID:90301487; PMID:2362815
A;Accession: S10246
A;Molecule type: mRNA
A;Residues: 1-434 <RAG>
A;Cross-references: UNIPROT:P17182; EMBL:X52379; NID:955490; PIDN:CAA3605.1; PID:g55491
R;Bottillico, L.A.; Kendrick, N.C.; Keller, A.; Li, Y.; Tabar, I.
Arterioscler. Thromb. 13, 261-275, 1993
A;Title: Choleatearyl ester loading of mouse peritoneal macrophages is associated with ch
soform.
A;Reference number: A56781; MUID:93152553; PMID:8427861
A;Accession: A56781
A;Status: preliminary
A;Molecule type: protein
A;Residues: 'X', '60', 'X', '62-67', 'X', '69-71', 'XX', '100-109', 'X', '111-112', 'X', '114', 'X', '184-185', 'X',
A;Experimental source: peritoneal macrophage
A;Note: Sequence modified after extraction from NCBI backbone
C;Superfamily: enolase
C;Keywords: carbon-oxygen lyase; gluconeogenesis; glycolysis; hydro-lyase
Query Match 80.7%; Score 67; DB 2; Length 434;
Best Local Similarity 81.2%; Pred. No. 0.00045;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 LWVGCTXQIKTGAPC 16
Db 384 LWVGCTQIKTGAPC 399

RESULT 12

S10247
phosphopyruvate hydratase (EC 4.2.1.11) gamma - mouse
N;Alternate names: 2-phosphoglycerate dehydratase; enolase gamma
C;Species: Mus musculus (house mouse)
C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 09-Jul-2004
C;Accession: S10247
R;Kaghad, M.; Dumont, X.; Chalon, P.; Lelias, J.M.; Lamande, N.; Lucas, M.; Lazar, M.; C
Nucleic Acids Res. 18, 3638, 1990
A;Title: Nucleotide sequences of cDNAs alpha and gamma enolase mRNAs from mouse brain.
A;Reference number: S10247
A;Accession: S10247
A;Molecule type: mRNA
A;Residues: 1-434 <RAG>
A;Cross-references: UNIPROT:P17183; EMBL:X52380; NID:955494; PIDN:CAA3606.1; PID:g55495
C;Superfamily: enolase
C;Keywords: carbon-oxygen lyase; gluconeogenesis; glycolysis; hydro-lyase
Query Match 80.7%; Score 67; DB 2; Length 434;
Best Local Similarity 81.2%; Pred. No. 0.00045;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

RESULT 13

S02072
 phosphopyruvate hydratase (EC 4.2.1.11) beta - rat
 N;Alternate name: enolase beta; enolase; muscle-specific
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 09-Jul-2004
 R;Ohshima, Y.; Mitsui, H.; Takayama, Y.; Kubhiya, E.; Sakimura, K.; Takahashi, Y.
 FEBS Lett. 242, 425-430, 1989
 A;Title: cDNA cloning and nucleotide sequence of rat muscle-specific enolase (beta-beta
 A;Reference number: S02072; MUID:8912113; PMID:2914621
 A;Accession: S02072
 A;Molecule type: mRNA
 A;Residues: 1-434 <OHS>
 A;Cross-references: UNIPROT:P15429; EMBL:Y00979; NID:957781; PIDN:CAA68788_1; PID:957782
 A;Note: the sequence from Fig. 4 is inconsistent with that from Fig. 2 in having 40-AAP
 C;Superfamily: enolase
 C;Keywords: carbon-oxygen lyase; gluconeogenesis; glycolysis; hydro-lyase; muscle

Query Match 80.7%; Score 67; DB 2; Length 434;
 Best Local Similarity 81.2%; Pred. No. 0.00045; Mismatches 3; Indels 0; Gaps 0;
 Matches 13; Conservative 0;

Oy 1 LVVGLCTXQIKTGPC 16
 Db 384 LVVGLCTXQIKTGPC 399

RESULT 14
 A29170
 phosphopyruvate hydratase (EC 4.2.1.11) alpha - human
 N;Alternate name: 2-phosphoglycerate dehydratase; enolase 1; enolase alpha
 C;Species: Homo sapiens (man)
 C;Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 16-Aug-2004
 C;Accession: S11696; A29170; S55858; A39183
 R;Giallongo, A.; Oliva, D.; Cali, L.; Barba, G.; Barbieri, G.; Feo, S.
 Eur. J. Biochem. 190, 567-573, 1990
 A;Title: Structure of the human gene for alpha-enolase.
 A;Reference number: S11696; MUID:90323004; PMID:2373081
 A;Status: nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-434 <GIM>
 A;Cross-references: UNIPROT:P06733; EMBL:X16288; NID:931172; PIDN:CAA34360_1; PID:91678
 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1989
 R;Giallongo, A.; Feo, S.; Moore, R.; Croce, C.M.; Showe, L.C.
 Proc. Natl. Acad. Sci. U.S.A. 83, 6641-6645, 1986
 A;Title: Molecular cloning and nucleotide sequence of a full-length cDNA for human alpha
 A;Reference number: A29170; MUID:86513654; PMID:3529090
 A;Accession: A29170
 A;Molecule type: mRNA
 A;Residue: 1-434 <GL2>
 A;Cross-references: GB:M14228; NID:g182113; PIDN:AAA52387_1; PID:g182114
 A;Note: the authors translated the codon AAG for residue 193 as His
 R;Walter, M.; Leidenberger, F.A.; Scheppe, K.W.; Berg, H.; Northemann, W.
 Submitted to the EMBL Data Library, February 1995
 A;Description: Auto-reactive epitopes within the human alpha-enolase and their recognition
 A;Reference number: S52858
 A;Accession: S52858
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-251, S, 253-434 <WAL>
 A;Cross-references: EMBL:94907; NID:9693932; PIDN:CAA59331_1; PID:g693933
 A;Experimental source: endometrium carcinoma cell line HRC-1B
 R;Miles, L.A.; Dahlberg, C.M.; Plescia, J.; Relez, J.; Kato, K.; Plow, B.F.
 Biochemistry 30, 1682-1691, 1991
 A;Title: Role of cell-surface lysines in plasminogen binding to cells: identification of
 A;Reference number: A39183; MUID:9129243; PMID:1847072
 A;Accession: A39183
 A;Molecule type: protein
 A;Residues: 170-182, T, 184, R, 186-190; 245-252 <ML>
 C;Genetics:
 A;Gene: GDI1
 A;Cross-references: GDB:119871; OMIM:172430

A;Map position: 1p36-1p36
 A;Introns: 29/1, 61/1; 80/3; 104/1; 148/3; 223/1; 289/1; 356/2; 392/3; 412/2
 C;Function:
 C;Description: catalyzes the reversible hydration of phosphoenolpyruvate to 2-phosphogly
 C;Superfamily: Enolase
 C;Keywords: Carbon-oxygen lyase; gluconeogenesis; glycolysis; hydro-lyase; magnesium
 F;P-2434/Product: phosphopyruvate hydratase alpha #status predicted <MAT>
 Query Match 80.7%; Score 67; DB 2; Length 434;
 Best Local Similarity 81.2%; Pred. No. 0.00045; Mismatches 3; Indels 0; Gaps 0;
 Matches 13; Conservative 0;

Oy 1 LVVGLCTXQIKTGPC 16
 Db 384 LVVGLCTXQIKTGPC 399

RESULT 15
 A32132
 phosphopyruvate hydratase (EC 4.2.1.11) alpha - duck
 N;Alternate name: enolase alpha; tau-crystallin
 C;Species: Anas platyrhynchos (domestic duck)
 C;Date: 21-May-1990 #sequence_revision 21-May-1990 #text_change 16-Aug-2004
 C;Accession: A32132
 C;Cross-references: A32132
 A;Title: Tau-crystallin/alpha-enolase: one gene encodes both an enzyme and a lens struc
 A;Reference number: A92750; MUID:89079778; PMID:2462567
 A;Accession: A32132
 A;Molecule type: mRNA
 A;Residues: 1-434 <WLS>
 A;Cross-references: UNIPROT:P19140; GB:X14195; NID:962455; PIDN:CAA32409_1; PID:962456
 C;Superfamily: Enolase
 C;Keywords: carbon-oxygen lyase; gluconeogenesis; glycolysis; hydro-lyase

Query Match 80.7%; Score 67; DB 2; Length 434;
 Best Local Similarity 81.2%; Pred. No. 0.00045; Mismatches 3; Indels 0; Gaps 0;
 Matches 13; Conservative 0;

Oy 1 LVVGLCTXQIKTGPC 16
 Db 384 LVVGLCTXQIKTGPC 399

Search completed: July 13, 2005, 12:13:59
 Job time : 39 sec_B

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QY 1 LVVGLCTXQIKTGpac 16
 XX ||||| ||||| |||||
 Db 1 LVVGLCTXQIKTGpac 16

RESULT 2
 AAY43197
 ID AAY43197 standard; peptide; 17 AA.
 XX
 AC AAY43197;
 XX DT 11-JAN-2000 (first entry)
 XX DR Schizophrenic derived antibody binding epitope #7.
 XX KW Schizophrenic derived antibody; binding epitope; schizophrenia;
 XX Platelet-associated antibody; diagnosis.
 XX OS Synthetic.
 XX PN WO951725-A2.
 XX PD 14-OCT-1999.
 XX PP 30-MAR-1999; 99WO-IL000190.
 XX PR 02-APR-1998; 98IL-00123925.
 XX PA (YEDA) YEDA RES & DEV CO LTD.
 XX PI Shinitzky M, Deckmann M;
 XX DR WPI; 1999-611037/52.

PT New peptides useful for diagnosis of schizophrenia.
 XX PS Claim 2; Page 21; 37pp; English.

XX CC This sequence is a peptide of the invention, which binds antibodies found in elevated levels in body fluids of schizophrenic patients. The peptide is useful in an assay for the diagnosis of schizophrenia, by binding the peptide to a platelet-containing fraction of blood, or a fraction containing platelet-associated antibodies (PAA) shed from the platelets, or preferably whole blood. The new peptides are able to differentiate between plasma samples from schizophrenic and non-schizophrenic patients, and can do so without having to first isolate the platelet-associated antibodies (PAA) fraction.

XX SQ Sequence 16 AA;

Query Match 95.2%; Score 79; DB 2; Length 16;
 Best Local Similarity 93.8%; Pred. No. 1.2e-05;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LVVGLCTXQIKTGpac 16
 Db 1 LVVGLCTXQIKTGpac 16

RESULT 4
 AAY43198
 ID AAY43198 standard; peptide; 17 AA.
 XX AC AAY43198;
 XX DT 11-JAN-2000 (first entry)
 XX DR Schizophrenic derived antibody binding epitope #8.
 XX KW Schizophrenic derived antibody; binding epitope; schizophrenia;
 XX Platelet-associated antibody; diagnosis.
 XX OS Synthetic.
 XX PN WO951725-A2.
 XX PD 14-OCT-1999.
 XX PP 30-MAR-1999; 99WO-IL000190.
 XX PR 02-APR-1998; 98IL-00123925.
 XX PA (YEDA) YEDA RES & DEV CO LTD.
 XX PI Shinitzky M, Deckmann M;
 XX DR WPI; 1999-611037/52.

PT New peptides useful for diagnosis of schizophrenia.
 XX PS Claim 3; Page 21; 37pp; English.

CC This sequence is a peptide of the invention, which binds antibodies found in elevated levels in body fluids of schizophrenic patients. The peptide is useful in an assay for the diagnosis of schizophrenia, by binding the peptide to a platelet-containing fraction of blood, or a fraction containing platelet-associated antibodies (PAA) shed from the platelets, or preferably whole blood. The new peptides are able to differentiate between plasma samples from schizophrenic and non-schizophrenic patients, and can do so without having to first isolate the platelet-associated antibodies (PAA) fraction.

CC Sequence 17 AA;

Query Match 96.4%; Score 80; DB 2; Length 17;
 Best Local Similarity 93.8%; Pred. No. 8.7e-06;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LWNGLCIXXQIKTGpac 16
 Db 1 LWNGLCIXXQIKTGpac 16

RESULT 3
 AAY43191
 ID AAY43191 standard; peptide; 16 AA.
 XX
 AC AAY43191;
 XX DT 11-JAN-2000 (first entry)
 XX DE Schizophrenic derived antibody binding epitope #1.
 XX KW Schizophrenic derived antibody; binding epitope; schizophrenia;
 XX Platelet-associated antibody; diagnosis.

xx
 cc This sequence is a peptide of the invention, which binds antibodies found
 cc in elevated levels in body fluids of schizophrenic patients. The peptide
 cc is useful in an assay for the diagnosis of schizophrenia, by binding the
 peptide to a platelet-containing fraction of blood, or a fraction
 containing Platelet-associated antibodies (PAA) shed from the platelets,
 or preferably whole blood. The new peptides are able to differentiate
 between plasma samples from schizophrenic and non-schizophrenic patients,
 cc and can do so without having to first isolate the platelet-associated
 antibodies (PAA) fraction
 xx
 SQ Sequence 17 AA:

Query Match	95.2%	Score	79;	DB	2;	Length	17;
Best Local Similarity	93.8%	Pred.	No.	1.3e-05		Mismatches	1;
Matches	15;	Conservative	0;			Indels	0;
Ov	1	LWVGGLCTQKTCGPAC	16				
Db	1	LWVGGLCTQKTCGPAC	16				

RESULT 5
 AAG79784
 ID AAG79784 standard; protein; 458 AA.
 XX
 AC AAG79784;
 XX
 DT 16-APR-2003 (first entry)
 XX
 DB Carbohydrate-associated protein (CHOP)-6.
 XX
 KW Human; carbohydrate associated polypeptides; CHOP; cancer;
 KW carbohydrate metabolism; diabetes; anaemia; hypoglycaemia; obesity;
 KW glycogen storage disease; neurological dysfunction; gene therapy;
 KW cell proliferation; actinic keratosis; arteriosclerosis; inflammation;
 KW atherosclerosis; cirrhosis; hepatitis; psoriasis; autoimmune disorder;
 KW acquired immunodeficiency syndrome; AIDS; humanized; transgenic;
 KW Addison's disease; allergy; asthma; contact dermatitis; bronchitis; gout;
 KW Hashimoto's thyroiditis; infection; reproduction; endometriosis;
 KW polycystic ovary syndrome; ovarian hyperstimulation syndrome;
 KW Down syndrome; cystic fibrosis; sickle cell anaemia; thalassemia;
 KW myocarditis; cardiomyopathy; Alzheimer's disease; Parkinson's disease;
 KW dementia; depression; epilepsy; Tourette's disorder; schizophrenia;
 KW central nervous system; cerebral palsy; mood; anxiety; knockin.
 XX
 OS Homo sapiens.

PH Key
 PT Peptide
 Location/Qualifiers
 1. .45
 /label= Enolase
 /note= "Identified by BLAST_BLOCKS"
 1..293
 /label= Enolase lyase
 /note= "Identified by BLAST_BLOCKS"
 2. .456
 /label= Endonuclease
 /note= "Identified by HMMER_PFM"
 2..456
 /label= Enolase
 /note= "Identified by BLAST_DOMO"
 7..456
 /label= Enolase
 /note= "Identified by BLAST_DOMO"
 113..129
 /label= Enolase signature
 /note= "Identified by BLIMPS_PRINTS"
 13..129
 /label= Enolase signature
 /note= "Identified by BLIMPS_PRINTS"

FT Protein
 FT
 Peptide
 FT
 Peptide
 FT Protein
 PR 22-MAY-2002; 2002WO-US018354.
 XX
 PR 25-MAY-2001; 2001US-0293768P.
 XX
 PR 01-AUG-2001; 2001US-0309548P.
 PR 23-AUG-2001; 2001US-0314460P.
 PR 19-OCT-2001; 2001US-0343706P.
 PR 07-DEC-2001; 2001US-033799P.
 XX
 PA (INCYT INCYSTE GENOMICS INC.
 XX
 PI Swarnakar A, Gervad AE, Hafalia AJA, Duggan BM, Emerling BM;
 PI Ison CH, Nguyen DB, Lee EA, Yue H, Yue H, Forsythe IJ, Li JX;
 PI Thangavelu K, Malia NK, Burford N, Mason PM, Lal PG, Lee S;
 PI Becha SD, Tang YT;
 XX
 DR WPI; 2003-140462/13.
 DR N-PSDB; ABA00836.
 XX
 PR Novel human carbohydrate associated polypeptide, useful in diagnosis,
 PR treatment and prevention of carbohydrate metabolism, cell proliferative,
 PR autoimmune/inflammatory, reproductive, and neurological disorders.
 XX
 PS Claim 1; Page 129-30; 141P; English.

CC The sequences given in AAG79784-88 represent human carbohydrate
 CC associated polypeptides (CHOP). The CHOP polypeptides and the nucleotide
 CC sequences encoding them, are useful for diagnosing, treating and
 CC preventing cancer, carbohydrate metabolic disorders (e.g. diabetes,
 CC anaemia, hypoglycaemia, obesity, glycogen storage disease, neurological
 CC dysfunctions), cell proliferative disorders (e.g. actinic keratosis,
 CC arteriosclerosis, atherosclerosis, cirrhosis, hepatitis, psoriasis),
 CC autoimmune/inflammatory disorders (such as acquired immunodeficiency

CC syndrome (AIDS), Addison's disease, allergies, asthma, contact dermatitis, bronchitis, gout, Hashimoto's thyroiditis), viral, bacterial, CC fungal, parasitic, protozoal and helminthic infections, reproductive disorder (e.g. endometriosis, polycystic ovary syndrome, ovarian fibrosis, sickle cell anaemia, thalassemia), cardiac disorders (e.g. myocarditis, cardiomyopathy), neurological disorders (e.g. Alzheimer's disease, Parkinson's disease, dementia, depression, epilepsy, Tourette's disorder, schizophrenia) and developmental disorders of central nervous system (e.g. cerebral palsy), mental disorders (e.g. mood, anxiety). CHOP proteins are useful in a number of drug screening techniques, and to analyse the proteome of a tissue or cell type. CHOP cDNA is useful for creating "knockin" humanized animals or transgenic animals to model human diseases, in somatic or germline gene therapy, to generate a transcript image of a tissue or cell type, for detecting differences in the chromosomal location due to translocation, inversion, etc., among normal, carrier or affected individuals, and as hybridization probes for mapping naturally occurring genomic sequences

SQ Sequence 458 AA;

Query Match	Score	DB	Length
Best Local Similarity	91.6%	6	458
Matches	14;	Pred. No.	0.0008;
Conservative	87.5%	Mismatches	2;
		Indels	0;
		Gaps	0;

QY 1 LNVGLCTXQIKTGpac 16
ID ADQ30526
DB 407 LNVGLCTXQIKTGpac 422

RESULT 6

ID	Accession	Sequence
ADQ30526	ADQ30526	standard; protein; 458 AA.
XX	XX	
AC	AC	
DT	DT	
XX	XX	
DS	DS	
Pancreas	Pancreas	cancer marker - alpha enolase.
XX	XX	
KW	KW	cytostatic; diagnosis; pancreatic cancer; antibody; antisense construct; differential expression.
OS	OS	Homo sapiens.
XX	XX	
PN	PN	WO2004055319-A2.
XX	XX	
PD	PD	01-JUN-2004.
XX	XX	
PP	PP	11-DEC-2003; 2003WO-BP014057.
XX	XX	
PR	PR	17-DEC-2002; 2002EP-00028058.
XX	XX	
PR	PR	05-NOV-2003; 2003EP-00025237.
XX	XX	
PA	(HOFF) HOFFMANN LA ROCHE & CO AG F.	
PA	(SINO-) SINOGENOMAX CO LTD CHINESE NAT HUMAN GEN.	
XX	XX	
PT	Chen J, Hu L, Liu TH, Lu ZH, Shen Y;	
XX	XX	
DR	WPI; 2004-488121/46.	
XX	XX	
PT	New specific markers comprises at least one polypeptide up-regulated in pancreatic cancer, useful for diagnosing pancreatic cancer.	
PT	Claim 1; SEQ ID NO 13; 301pp; English.	
XX	XX	
The invention relates to a marker (I) for diagnosis of pancreatic cancer comprising at least one polypeptide selected from 55 proteins up-regulated in pancreatic cancer (Table 2 and Table 3, given in the specification) or from 68 proteins with higher levels in pancreatic cancer compared to normal tissue (Table 6, given in the specification).		
(I) is a polypeptide for use as a marker or as a component of a marker for diagnosis of pancreatic cancer and/or the susceptibility to		

CC pancreatic cancer. A compound (antibody, an antibody-derivative, an antibody fragment, a peptide, or an antisense construct) identified by CC screening methods using (I) is useful for treatment or prevention of CC pancreatic cancer. It is also useful for the preparation of a diagnostic CC composition for diagnosing pancreatic cancer or a predisposition for CC pancreatic cancer. The current polypeptides were found to be CC differentially expressed in pancreatic tissue obtained from individuals CC suffering from pancreatic cancer as compared to healthy pancreatic CC tissue. They have been identified as suitable as markers of pancreatic CC cancer for early diagnosis of the disease. This sequence corresponds to a CC protein marker of the invention.

SQ Sequence 458 AA;

Query Match	Score	DB	Length
Best Local Similarity	91.6%	8	458
Matches	14;	Pred. No.	0.0008;
Conservative	87.5%	Mismatches	2;
		Indels	0;
		Gaps	0;

QY 1 LNVGLCTXQIKTGpac 16
ID AAY43202
DB AAY43202
XX AAY43202;
XX DT 11-JAN-2000 (first entry)
XX DE Schizophrenic derived antibody binding epitope #12.
XX KW Schizophrenic derived antibody; binding epitope; schizophrenia; platelet-associated antibody; diagnosis.
XX OS Synthetic.
XX PN WO951725-A2.
XX PD 14-OCT-1999.
XX PP 30-MAR-1999; 99WO-IL000190.
XX BR 02-APR-1998; 98IL-00123925.
XX PA (YEDA) YEDA RES & DEV CO LTD.
XX PI Shinitzky M, Deckmann M;
XX DR WPI; 1999-611037/52.
XX PT New peptides useful for diagnosis of schizophrenia.
XX PS Claim 4; Page 21; 37pp; English.

XX This sequence is a peptide of the invention, which binds antibodies found in elevated levels in body fluids of schizophrenic patients. The peptide is useful in an assay for the diagnosis of schizophrenia, by binding the peptide to a platelet-containing fraction of blood, or a fraction containing platelet-associated antibodies (PAA) shed from the platelets, or preferably whole blood. The new peptides are able to differentiate between plasma samples from schizophrenic and non-schizophrenic patients, and can do so without having to first isolate the platelet-associated antibodies (PAA) fraction

SQ Sequence 16 AA;

Query Match	Score	DB	Length
Best Local Similarity	80.7%	2	16
Matches	13;	Pred. No.	0.00099;
Conservative	81.2%	Mismatches	3;
		Indels	0;
		Gaps	0;

QY 1 LNVGLCTXQIKTGpac 16

CC in elevated levels in body fluids of schizophrenic patients. The peptide CC is useful in an assay for the diagnosis of schizophrenia, by binding the CC peptide to a platelet-containing fraction of blood, or a fraction containing platelet-associated antibodies (PAA) shed from the platelets, CC or preferably whole blood. The new peptides are able to differentiate CC between plasma samples from schizophrenic and non-schizophrenic patients, CC and can do so without having to first isolate the platelet-associated antibodies (PAA) fraction.

SQ Sequence 19 AA;

Query Match 80.7%; Score 67; DB 2; Length 19;
Best Local Similarity 81.2%; Pred. No. 0.0012; 0; Mismatches 3; Indels 0; Gaps 0;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 LVVGLCTXQIKTGAPC 16
DB 3 LVVGLCTGQIKTGAPC 18

RESULT 11

AY43193 ID AY43193 standard; peptide; 20 AA.
XX AC AY43193;
XX DT 11-JAN-2000 (first entry)

XX DB Schizophrenic derived antibody binding epitope #2.

XX KW schizophrenic derived antibody; binding epitope; schizophrenia;
XX platelet-associated antibody; diagnosis.

XX OS synthetic.

XX PN WO951725-A2.

XX PD 14-OCT-1999.
XX PP 30-MAR-1999; 99WO-IL000190.

XX BR 02-APR-1998; 98IL-00123925.

XX PA (YEDA) YEDA R&D & DEV CO LTD.

XX PI Shinitzky M, Deckmann M;

XX DR WPI; 1999-611037/52.

XX PT New peptides useful for diagnosis of schizophrenia.
XX PS Claim 3; Page 21; 37pp; English.

CC This sequence is a peptide of the invention, which binds antibodies found CC in elevated levels in body fluids of schizophrenic patients. The peptide CC is useful in an assay for the diagnosis of schizophrenia, by binding the peptide to a platelet-containing fraction of blood, or a fraction containing platelet-associated antibodies (PAA) shed from the platelets, CC or preferably whole blood. The new peptides are able to differentiate CC between plasma samples from schizophrenic and non-schizophrenic patients, CC and can do so without having to first isolate the platelet-associated CC antibodies (PAA) fraction.

XX SQ Sequence 28 AA;

Query Match 80.7%; Score 67; DB 2; Length 28;
Best Local Similarity 81.2%; Pred. No. 0.0017; 0; Mismatches 3; Indels 0; Gaps 0;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 LVVGLCTXQIKTGAPC 16
DB 12 LVVGLCTGQIKTGAPC 27

RESULT 13

ABU04377 ID ABU04377 standard; protein; 269 AA.
XX AC ABU04377;
XX DT 29-JAN-2003 (first entry)

XX DB Human expressed protein tag (EPT) #1043.

XX Translational profiling; expressed protein tag; EPT; kinase; phosphatase; protease; protease inhibitor; transporter; cytoskeletal protein; receptor; transcription factor; cancer; MHC; major histocompatibility complex; myeloma; colon cancer; gastric cancer; adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.

XX OS Homo sapiens.

XX SQ Sequence 20 AA;

Query Match 80.7%; Score 67; DB 2; Length 20;
Best Local Similarity 81.2%; Pred. No. 0.0012; 0; Mismatches 3; Indels 0; Gaps 0;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 LVVGLCTXQIKTGAPC 16
DB 4 LVVGLCTGQIKTGAPC 19

PN WO200278524-A2.
 XX
 PD 10-OCT-2002.
 XX
 PR 28-MAR-2002; 2002WO-US009671.
 XX
 PR 28-MAR-2001; 2001US-0279495P.
 PR 21-MAY-2001; 2001US-029254P.
 PR 08-AUG-2001; 2001US-031001P.
 PR 01-OCT-2001; 2001US-0326370P.
 PR 04-DEC-2001; 2001US-033670P.
 PR 20-FEB-2002; 2002US-0358985P.
 XX
 PA (ZYCO-) ZYCOS INC.
 XX
 PI Chicz RM, Tomlinson AJ, Urban RG;
 XX
 DR WPI; 2003-040607/03.
 XX
 PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters, cytoskeletal proteins, receptors or transcription factors), useful for treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or leukemia.
 XX
 PS Example 2; SEQ ID NO 1043; 134pp; English.
 XX
 CC The invention describes a purified polypeptide, which comprises a fragment of a kinase, phosphatase, protease, protease inhibitor, transporter, cytoskeletal protein, receptor or transcription factor. The polypeptide is useful as an immunogenic composition for eliciting in a mammal an immune response directed against any of the purified polypeptide, or the antibody that binds to this polypeptide. The purified polypeptide, or the antibody that binds to this polypeptide, is useful for treating cancer. The polypeptide is also useful for identifying compounds that binds to a naturally processed class I or class II MHC-binding polypeptide. The polypeptides and polynucleotides are particularly useful for treating or preventing myeloma, colon cancer, adenocarcinoma, sarcoma, melanoma, lymphoma or leukaemia. These are also useful for screening agents for treating the above mentioned diseases. This sequence represents an expressed protein tag (EPT) isolated from human tissue for translational profiling. Note: This sequence does not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 269 AA;

Query Match	80.7%	Score	67	DB	6	Length	269;
Best Local Similarity	81.2%	Pred.	No.	0.014			
Matches	13	;	Mismatches	0			
Qy	1	LVGLCTQIQKIGPAC	16				
D _b	219	LVGLCTQIQKIGPAC	234				

RESULT 14

ABU04378	ID	ABU04378	standard; protein; 272 AA.
XX	XX	XX	
AC	AC	AC	
XX	XX	XX	
DT	29-JAN-2003	(first entry)	
XX	XX	XX	
DB	Human expressed protein tag (EPT) #1044.		

XX Translational profiling; expressed protein tag; EPT; kinase; phosphatase; protease; protease inhibitor; transporter; cytoskeletal protein; receptor; transcription factor; cancer; MHC; major histocompatibility complex; myeloma; colon cancer; gastric cancer; adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.

XX OS Homo sapiens.

XX

PN WO200278524-A2.
 XX
 PD 10-OCT-2002.
 XX
 PR 28-MAR-2002; 2002WO-US009671.
 XX
 PR 28-MAR-2001; 2001US-0279495P.
 PR 21-MAY-2001; 2001US-029254P.
 PR 08-AUG-2001; 2001US-031001P.
 PR 01-OCT-2001; 2001US-0326370P.
 PR 04-DEC-2001; 2001US-033670P.
 PR 20-FEB-2002; 2002US-0358985P.
 XX
 PA (ZYCO-) ZYCOS INC.
 XX
 PI Chicz RM, Tomlinson AJ, Urban RG;
 XX
 DR WPI; 2003-040607/03.
 XX
 PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters, cytoskeletal proteins, receptors or transcription factors), useful for treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or leukemia.
 XX
 PS Example 2; SEQ ID NO 1044; 134pp; English.
 XX
 CC The invention describes a purified polypeptide, which comprises a fragment of a kinase, phosphatase, protease inhibitor, transporter, cytoskeletal protein, receptor or transcription factor. The polypeptide is useful as an immunogenic composition for eliciting in a mammal an immune response directed against any of the purified polypeptide. The purified polypeptide, or the antibody that binds to this polypeptide, is useful for treating cancer. The polypeptide is also useful for identifying compounds that binds to a naturally processed class I or class II MHC-binding polypeptide. The polypeptides and polynucleotides are particularly useful for treating or preventing myeloma, colon cancer, adenocarcinoma, sarcoma, melanoma, lymphoma or leukaemia. These are also useful for screening agents for treating the above mentioned diseases. This sequence represents an expressed protein tag (EPT) isolated from human tissue for translational profiling. Note: This sequence does not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 272 AA;

Query Match	80.7%	Score	67	DB	6	Length	272;
Best Local Similarity	81.2%	Pred.	No.	0.014			
Matches	13	;	Mismatches	0			
Qy	1	LVGLCTQIQKIGPAC	16				
D _b	222	LVGLCTQIQKIGPAC	237				

RESULT 15

ABU04375	ID	ABU04375	standard; protein; 272 AA.
XX	XX	XX	
AC	AC	AC	
XX	XX	XX	
DT	29-JAN-2003	(first entry)	
XX	XX	XX	
DB	Human expressed protein tag (EPT) #1041.		

XX Translational profiling; expressed protein tag; EPT; kinase; phosphatase; protease; protease inhibitor; transporter; cytoskeletal protein; receptor; transcription factor; cancer; MHC; major histocompatibility complex; myeloma; colon cancer; gastric cancer; adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.

XX OS Homo sapiens.

XX

PN WO200278524-A2.
 XX
 PD 10-OCT-2002.
 XX
 PF 28-MAR-2002; 2002WO-US009671.
 XX
 PR 28-MAR-2001; 2001US-0279495P.
 PR 21-MAY-2001; 2001US-0292543P.
 PR 08-AUG-2001; 2001US-0310801P.
 PR 01-OCT-2001; 2001US-0326370P.
 PR 04-DEC-2001; 2001US-0336780P.
 PR 20-FEB-2002; 2002US-0358955P.
 XX
 PA (ZYCO-) ZYCO'S INC.
 XX
 PT CHICZ RM, Tomlinson AJ, Urban RG;
 DR
 WPI; 2003-040607/03.
 XX
 PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters, cytoskeletal proteins, receptors or transcription factors), useful for treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or leukemia.
 XX
 PS Example 2; SEQ ID NO 1041; 134PP; English.
 XX
 CC The invention describes a purified polypeptide, which comprises a fragment of a kinase, phosphatase, protease, protease inhibitor, transporter, cytoskeletal protein, receptor or transcription factor. The polypeptide is useful as an immunogenic composition for eliciting in a mammal an immunogenic response directed against any of the purified polypeptide. The purified polypeptide, or the antibody that binds to this polypeptide, is useful for treating cancer. The polypeptide is also useful for identifying compounds that binds to a naturally processed class I or class II MHC-binding polypeptide. The polypeptides and polynucleotides are particularly useful for treating or preventing myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma, lymphoma or leukaemia. These are also useful for screening agents for treating the above mentioned diseases. This sequence represents an expressed protein tag (EPT) isolated from human tissue for translational profiling. Note: This sequence does not appear in the printed specification but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
 CC
 XX
 SQ Sequence 272 AA;

Query Match 80.7%; Score 67; DB 6; Length 272;
 Best Local Similarity 81.2%; Pred. No. 0.014;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy	1	LVNGLCTRQIKTGAPC 16
Db	222	LVNGLCTRQIKTGAPC 237

Search completed: July 13, 2005, 12:12:13
 Job time : 162 secs

GenCore version 5.1.5
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OM protein - protein search, using sw model

Run on: July 13, 2005, 12:06:44 ; Search time 41 Seconds
 (without alignment time)
 30.952 Million cell updates/sec

Title:	US-09-647-457-E-1
Perfect Score:	83
Sequence:	1 LIVVGLCTQIKTGPACK 17
Scoring table:	BLOSUM62
Gapop:	Gapop 10.0 , Gapext 0.5
Searched:	513545 seqs, 7649064 residues
Total number of hits satisfying chosen parameters:	513545
Minimum DB seq length:	0
Maximum DB seq length:	200000000
Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	
Database :	Issued Patents AA:*
	1: /cgn2_6/pctodata/1/iaa/5A_COMB.pep:*
	2: /cgn2_6/pctodata/1/iaa/5B_COMB.pep:*
	3: /cgn2_6/pctodata/1/iaa/6A_COMB.pep:*
	4: /cgn2_6/pctodata/1/iaa/6B_COMB.pep:*
	5: /cgn2_6/pctodata/1/iaa/PCTUS_COMB.pep:*
	6: /cgn2_6/pctodata/1/iaa/backfilest1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
1	67	80.7	434	4 US-09-949-016-6153	Sequence 6153, Ap
2	67	80.7	433	4 US-09-949-016-6159	Sequence 6159, Ap
3	44	53.0	444	4 US-09-232-991A-2120	Sequence 7269, Ap
4	44	53.0	444	4 US-09-232-352-7269	Sequence 2354, Ap
5	44	53.0	445	4 US-09-550-236-2354	Sequence 1054, A
6	46.4	46.4	148	4 US-09-248-796A-17054	Sequence 65, Appl
7	38	45.8	37	2 US-09-248-839C-65	Sequence 110, Appl
8	38	45.8	233	4 US-09-216-393B-110	Sequence 2, Appl
9	38	45.8	511	3 US-09-105-039A-2	Sequence 4, Appl
10	38	45.8	530	3 US-09-105-039A-4	Sequence 22813, A
11	38	45.2	66	4 US-09-248-796A-2813	Sequence 348, App
12	37	44.6	127	4 US-09-711-164-348	Sequence 6090, Ap
13	37	44.6	456	4 US-09-543-681A-6090	Sequence 10061, A
14	37	44.6	459	4 US-09-489-039A-10061	Sequence 24, Appl
15	37	44.6	670	4 US-09-575-081B-24	Sequence 26, Appl
16	37	44.6	670	4 US-09-575-081B-26	Sequence 3, Appl
17	37	44.6	1886	3 US-09-938-105-3	Sequence 55, Appl
18	36	43.4	12	4 US-09-417-608A-55	Sequence 431, Appl
19	36	43.4	63	4 US-08-439-260A-431	Sequence 431, Appl
20	36	43.4	63	4 US-08-488-446-431	Sequence 431, Appl
21	36	43.4	63	4 US-08-467-341A-431	Sequence 431, Appl
22	36	43.4	63	4 US-08-224-550B-431	Sequence 431, App
23	36	43.4	108	4 US-09-328-352-5857	Sequence 5857, Ap
24	36	43.4	139	4 US-09-902-540-14334	Sequence 14334, A
25	36	43.4	211	4 US-09-370-767-36404	Sequence 36404, A
26	36	43.4	211	4 US-09-270-767-51621	Sequence 51621, A
27	36	43.4	238	4 US-09-232-991A-24386	Sequence 24386, A

ALIGNMENTS

RESULT 1	US-09-949-016-6153	Sequence 6153, Application US/09949016
GENERAL INFORMATION:	APPLICANT: VENTER, J. Craig et al.	
	TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF	
	FILE REFERENCE: CL001307	
	CURRENT APPLICATION NUMBER: US/09/949, 016	
	CURRENT FILING DATE: 2000-04-14	
	PRIOR APPLICATION NUMBER: 60/241, 755	
	PRIOR FILING DATE: 2000-10-20	
	PRIOR APPLICATION NUMBER: 60/237, 768	
	PRIOR FILING DATE: 2000-10-03	
	PRIOR APPLICATION NUMBER: 60/231, 498	
	PRIOR FILING DATE: 2000-09-08	
	NUMBER OF SEQ ID NOS: 207012	
	SOFTWARE: FASTSEQ for Windows Version 4.0	
	SEQ ID NO 6153	
	LENGTH: 434	
	TYPE: PRT	
	ORGANISM: Human	
RESULT 2	US-09-949-016-6159	Sequence 6159, Application US/09949016
Query Match	Best local Similarity : 81.2%; Score 67; DB 4; length 434; Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;	
OY	1 LIVVGLCTQIKTGPACK 16	Db 384 LIVVGLCTQIKTGPACK 399
	Sequence 8359, Application US/09949016	Patent No. 681239
	GENERAL INFORMATION:	APPLICANT: VENTER, J. Craig et al.
	TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF	FILE REFERENCE: CL001307
	CURRENT APPLICATION NUMBER: US/09/949, 016	CURRENT FILING DATE: 2000-04-14
	PRIOR APPLICATION NUMBER: 60/241, 755	PRIOR FILING DATE: 2000-10-20
	PRIOR APPLICATION NUMBER: 60/237, 768	PRIOR FILING DATE: 2000-10-03
	PRIOR APPLICATION NUMBER: 60/231, 498	PRIOR FILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-08
 NUMBER OF SEQ ID NOS: 207012
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 8359
 LENGTH: 443
 TYPE: PRT
 ORGANISM: Human
 US-09-949-016-8359
 RESULT 3
 Query Match 80.7%; Score 67; DB 4; Length 443;
 Best Local Similarity 81.2%; Pred. No. 0.0056; Mismatches 3; Indels 0; Gaps 0;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 LVVGLCTXQIKTGAPC 16
 Db 393 LVVGLCTXQIKTGAPC 408
 LENGTH: 443
 TYPE: PRT
 ORGANISM: Human
 US-09-252-991A-21020
 Sequence 21020, Application US/09252991A
 Patent No. 6551795
 GENERAL INFORMATION:
 APPLICANT: Marc J. Rubenfield et al.
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 FILE REFERENCE: 107196.136
 CURRENT APPLICATION NUMBER: US/09/252, 991A
 CURRENT FILING DATE: 1999-02-18
 PRIOR APPLICATION NUMBER: US 60/074, 788
 PRIOR FILING DATE: 1998-02-18
 PRIOR APPLICATION NUMBER: US 60/094, 190
 PRIOR FILING DATE: 1998-07-27
 NUMBER OF SEQ ID NOS: 33142
 SEQ ID NO: 21020
 LENGTH: 444
 TYPE: PRT
 ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-21020
 RESULT 4
 Query Match 53.0%; Score 44; DB 4; Length 444;
 Best Local Similarity 56.2%; Pred. No. 26; Mismatches 7; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
 QY 1 LVVGLCTXQIKTGAPC 16
 Db 397 LVVGLCTXQIKTGAPC 412
 LENGTH: 444
 TYPE: PRT
 ORGANISM: Pseudomonas aeruginosa
 US-09-328-352-7269
 Sequence 7269, Application US/09328352
 Patent No. 6562958
 GENERAL INFORMATION:
 APPLICANT: Gary L. Breton et al.
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
 FILE REFERENCE: GTC99-03.PA
 CURRENT APPLICATION NUMBER: US/09/328, 352
 CURRENT FILING DATE: 1999-06-04
 NUMBER OF SEQ ID NOS: 8252
 SEQ ID NO: 7269
 LENGTH: 444
 TYPE: PRT
 ORGANISM: Acinetobacter baumannii
 US-09-328-352-7269
 RESULT 5
 Query Match 80.7%; Score 67; DB 4; Length 443;
 Best Local Similarity 81.2%; Pred. No. 0.0056; Mismatches 3; Indels 0; Gaps 0;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 LVVGLCTXQIKTGAPC 16
 Db 393 LVVGLCTXQIKTGAPC 408
 LENGTH: 443
 TYPE: PRT
 ORGANISM: Human
 US-09-540-236-2354
 Sequence 2354, Application US/09540236
 Patent No. 66713910
 GENERAL INFORMATION:
 APPLICANT: Gary L. Bretton et al.
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR
 FILE REFERENCE: 2709-2005-001
 CURRENT APPLICATION NUMBER: US/09/540, 236
 CURRENT FILING DATE: 2000-04-04
 NUMBER OF SEQ ID NOS: 3840
 SEQ ID NO: 2354
 LENGTH: 445
 TYPE: PRT
 ORGANISM: M.catarrhalis
 US-09-540-236-2354
 RESULT 6
 Query Match 53.0%; Score 44; DB 4; Length 445;
 Best Local Similarity 56.2%; Pred. No. 26; Mismatches 7; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
 QY 1 LVVGLCTXQIKTGAPC 16
 Db 397 LVVGLCTXQIKTGAPC 412
 LENGTH: 445
 TYPE: PRT
 ORGANISM: M.catarrhalis
 US-09-248-796A-17054
 Sequence 17054, Application US/09248796A
 Patent No. 6747137
 GENERAL INFORMATION:
 APPLICANT: Keith Weinstock et al.
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
 FILE REFERENCE: 107196.132
 CURRENT APPLICATION NUMBER: US/09/248, 796A
 CURRENT FILING DATE: 1999-02-12
 PRIOR APPLICATION NUMBER: US 60/074, 725
 PRIOR FILING DATE: 1998-02-13
 PRIOR APPLICATION NUMBER: US 60/096, 409
 PRIOR FILING DATE: 1998-08-13
 NUMBER OF SEQ ID NOS: 28208
 SEQ ID NO: 17054
 LENGTH: 148
 TYPE: PRT
 ORGANISM: Candida albicans
 US-09-248-796A-17054
 RESULT 7
 Query Match 46.4%; Score 38.5; DB 4; Length 148;
 Best Local Similarity 68.8%; Pred. No. 68; Mismatches 3; Indels 1; Gaps 1;
 Matches 11; Conservative 1; Mismatches 3; Indels 1; Gaps 1;
 QY 1 LVVGLCTXQIKTG-PA 15
 Db 98 LVVGLRSQIKTGAPA 113
 LENGTH: 148
 TYPE: PRT
 ORGANISM: Candida albicans
 US-08-248-839C-65
 Sequence 839C-65, Application US/08248839C
 Patent No. 5843702
 GENERAL INFORMATION:
 APPLICANT: McConnell, David
 APPLICANT: Devine, Kevin
 APPLICANT: O'Kane, Charles
 TITLE OF INVENTION: A Gene Expression System
 NUMBER OF SEQUENCES: 185
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: No. 58437020 No. 5843702disk of No. 5843702th America, Inc.

STREET: 405 Lexington Avenue

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10174-6401

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/248,839C

FILING DATE: 25-MAY-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Gregg, Valeta A.

REGISTRATION NUMBER: 35,127

REFERENCE/DOCKET NUMBER: 3614,214-US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212-867-0123

TELEFAX: 212-878-9655

INFORMATION FOR SEQ ID NO: 65:

SEQUENCE CHARACTERISTICS:

LENGTH: 37 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: Protein

US-08-248-839C-65

Query Match Score 38; DB 2; Length 37;

Best Local Similarity 53.8%; Pred. No. 22;

Matches 7; Conservative 0; Mismatches 6;

Indels 0; Gaps 0;

Qy 4 GLCTXQIKTGAC 16

Db 18 GLCDLWKRGPGC 30

RESULT 8

US-09-216-393B-110

; Sequence 110. Application US/09216393B

; GENERAL INFORMATION:

; Patent No. 6514694

; APPLICANT: Milhausen, Michael James

; TITLE OF INVENTION: TOXOPLASMA GONDII PROTEINS, NUCLEAR ACID MOLECULES, AND USES THEREFOR

; FILE REFERENCE: TX-1-C2

; CURRENT APPLICATION NUMBER: US/09/216,393B

; PRIORITY FILING DATE: 1998-12-18

; PRIOR APPLICATION NUMBER: 09/994,825

; NUMBER OF SEQ ID NOS: 366

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO: 110

; LENGTH: 233

; TYPE: PRT

; ORGANISM: Toxoplasma gondii

US-09-216-393B-110

Query Match Score 38; DB 4; Length 233;

Best Local Similarity 50.0%; Pred. No. 1.3e+02;

Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 5 LCTXQIKTGAC 16

Db 3 VCEEKCKTGPGNC 14

RESULT 9

US-09-105-039A-4

; Sequence 2. Application US/09105039A

; Patent No. 6001806

; GENERAL INFORMATION:

; APPLICANT: Hilbert, David M.

; APPLICANT: Bednark, Daniel P.

; APPLICANT: Nardelli, Bernadetta

; APPLICANT: Murphy, Mariane

; APPLICANT: Parteelee, David

; APPLICANT: Gronowski, Ann

; APPLICANT: Schreiber, Robert

APPLICANT: Hilbert, David M.

APPLICANT: Bednark, Daniel P.

APPLICANT: Nardelli, Bernadetta

APPLICANT: Murphy, Mariane

APPLICANT: Parteelee, David

APPLICANT: Gronowski, Ann

APPLICANT: Schreiber, Robert

TITLE OF INVENTION: Interferon Stimulating Protein and Uses

TITLE OF INVENTION: Thereof

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: Human Genome Sciences, Inc

STREET: 9410 Key West Avenue

CITY: Rockville

STATE: MD
COUNTRY: US
ZIP: 20550
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/105,039A
FILING DATE:
CLASSIFICATION: 530
REFERENCE/DOCKET NUMBER: PB384
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-309-8504
TELEFAX: 301-309-8439
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 530 amino acids
TYPE: amino acid
STRANDBEADNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-105-039A-4

Query Match 45.8%; Score 38; DB 3; Length 530;
Best Local Similarity 66.7%; Pred. No. 2.7e+02; Mismatches 6; Conservative 1; Indels 0; Gaps 0;

Matches 6; Conservatve 1; Mismatches 2; Indels 0; Gaps 0;

Qy 6 CTXQKTKGP 14
Db 42 CNAQMKTG 50

RESULT 11
US-09-248-796A-22813
Sequence 22813, Application US/09248796A
Patent No. 6747137
GENERAL INFORMATION:
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEARIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107195_132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 22813
LENGTH: 66

TYPE: PRT
ORGANISM: Candida albicans
FEATURE:
NAME/KEY: UNSURE
LOCATION: (30)
OTHER INFORMATION: Identity of amino acid sequences at the above locations are unknc
US-09-248-796A-22813

Query Match 45.2%; Score 37.5; DB 4; Length 66;
Best Local Similarity 50.0%; Pred. No. 46; Mismatches 8; Conservative 2; Indels 1; Gaps 5;

Matches 8; Conservative 2; Mismatches 1; Indels 5; Gaps 1;

Qy 3 VLGCTKQ----IKTG 13
Db 48 IGLCTIOSAMISVKTG 63

RESULT 12
US-09-711-164-348
Sequence 348, Application US/09711164
Patent No. 6589738
GENERAL INFORMATION:
APPLICANT: Forsyth, R. Allyn
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
TITLE OF INVENTION: GENES ESSENTIAL FOR MICROBIAL PROLIFERATION AND ANTISENSE THRETTING
FILE REFERENCE: ELITRA.008A
CURRENT APPLICATION NUMBER: US/09/711,164
CURRENT FILING DATE: 2000-11-09
PRIORITY NUMBER: US 60/164415
PRIORITY FILING DATE: 1999-11-9
NUMBER OF SEQ ID NOS: 469
SOFTWARE: FastaSQ for Windows Version 4.0
SEQ ID NO 348
LENGTH: 127
TYPE: PRT
ORGANISM: Escherichia coli
US-09-711-164-348

Query Match 44.6%; Score 37; DB 4; Length 127;
Best Local Similarity 46.2%; Pred. No. 1e+02; Mismatches 6; Conservative 3; Indels 4; Gaps 0;

Matches 6; Conservatve 3; Mismatches 4; Indels 0; Gaps 0;

Qy 4 GLCTKQKTKGPAC 16
Db 33 GLTSKWKSRPQC 45

RESULT 13
US-09-543-681A-6090
Sequence 6090, Application US/09543681A
Patent No. 6605709
GENERAL INFORMATION:
APPLICANT: GARY BRETON
TITLE OF INVENTION: NUCLEARIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709_1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 6090
LENGTH: 456
TYPE: PRT
ORGANISM: Proteus mirabilis
US-09-543-681A-6090

Query Match 44.6%; Score 37; DB 4; Length 456;
Best Local Similarity 61.5%; Pred. No. 3.4e+02; Mismatches 8; Conservative 0; Indels 0; Gaps 0;

Matches 8; Conservatve 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 LVGCTKQKTKG 13
Db 407 LAVGTAAGQKTKG 419

RESULT 14
US-09-489-039A-10061
Sequence 10061, Application US/09489039A
Patent No. 6610836
GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEARIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709_2004-001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27

; PRIORITY APPLICATION NUMBER: US 60/117,747
; PRIORITY FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 10061
; LENGTH: 459
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-10061

Query Match 44.6%; Score 37; DB 4; Length 459;
Best Local Similarity 61.5%; Pred. No. 3.4e+02;
Matches 8; Conservative 0; Mismatches 5; Indels 0; Caps 0;
Qy 1 LVVGLCTKQIKTG 13
Db 410 LAVGTAAGQIKTG 422

RESULT 15
US-09-575-081B-24

; Sequence 24, Application US/09575081B

; Patent No. 669934

; GENERAL INFORMATION:

; APPLICANT: BRISTOL-MYERS SQUIBB COMPANY

; TITLE OF INVENTION: NOVEL ORGANIC ANION TRANSPORT PROTEINS

; FILE REFERENCE: DB23

; CURRENT APPLICATION NUMBER: US/09/575,081B

; CURRENT FILING DATE: 2000-05-19

; PRIOR APPLICATION NUMBER: 60/1135,081

; PRIOR FILING DATE: 1999-05-20

; NUMBER OF SEQ ID NOS: 29

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 24

; LENGTH: 670

; TYPE: PRT

; ORGANISM: Rat

Query Match 44.6%; Score 37; DB 4; Length 670;
Best Local Similarity 53.3%; Pred. No. 4.9e+02;
Matches 8; Conservative 1; Mismatches 2; Indels 4; Gaps 1;

Qy 2 VVGLCTKQIKTGpac 16
Db 496 VLGLC---KKGFBc 506

Search completed: July 13, 2005, 12:14:47
Job time : 43 sec8

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Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension .rup) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

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